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May 23, 2000

US-PAT-NO: 6066474DOCUMENT-IDENTIFIER: US 6066474 A

TITLE: Y2H56 A strong IKK binding protein

DATE-ISSUED: May 23, 2000

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APPL-NO: 09/ 195286 [PALM]

DATE FILED: November 18, 1998

INT-CL: [07] C12 P 21/06, C12 N 1/20, C07 H 21/04, C07 H 21/02, C07 H 1/00

US-CL-ISSUED: 435/69.1; 536/23.5, 536/23.1, 530/350, 435/252.3, 435/320.1

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 530/350, 536/23.1, 536/23.5

FIELD-OF-SEARCH: 435/69.1, 435/320.1, 435/252.3, 536/23.1, 536/23.5

PRIOR-ART-DISCLOSED:

U.S. PATENT DOCUMENTS

Search Selected

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	PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
<input type="checkbox"/>	<u>5776717</u>	July 1998	Cao	435/15
<input type="checkbox"/>	<u>5804374</u>	September 1998	Baltimore et al.	435/6

OTHER PUBLICATIONS

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Mock et al., "CHUK, a Conserved Helix-Loop-Helix Ubiquitous Kinase, Maps to Human Chromosome 10 and Mouse Chromosome 19", Genomics 27:348-351 (1995).

Margery A. Connelly and Kenneth B. Marcu, "CHUK, a New Member of the Helix-Loop-Helix and Leucine Zipper Families of Interacting Proteins, Contains a Serine-Threonine Kinase Catalytic Domain", Cellular and Molecular Biology Research 41:537-549 (1995).

Garkavtsev, et al., "Suppression of the novel growth inhibitor p33.sup.ING1 promotes neoplastic transformation", Nature Genetics 14:415-420 (1996).

DiDonato et al., "A Cytokine-Responsive I.kappa.B Kinase That Activates the Transcription Factor NF-.kappa.B", Nature 388:548-554 (1997).

Regnier et al., "Identification and Characterization of an I.kappa.B Kinase", Cell 90:373-383 (1997).

Ilana Stancovski and David Baltimore, "NF-.kappa.B Activation: The I.kappa.B Kinase Revealed?", Cell 91:299-302 (1997).

Woronicz et al., "I.kappa.B Kinase-.beta.: NF-.kappa.B Activation and Complex Formation with I.kappa.B Kinase-.alpha. and NIK", Science 278:866-869 (1997).

Zandi et al., "The I.kappa.B Kinase Complex (IKK) Contains Two Kinase Subunits, IKK.alpha. and IKK.beta., Necessary for I.kappa.B Phosphorylation and NF-.kappa.B Activation", Cell 91:243-252 (1997).

Garkavtsev, et al., "The candidate tumour suppressor p33.sup.ING1 cooperates with p53 in cell growth control", Nature 391:295-298 (1998).

Moshe Oren, "Teaming up to restrain cancer", Nature 391:233-234 (1998).

ART-UNIT: 162

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ABSTRACT:

The present invention provides an isolated I.kappa.B kinase binding protein designated Y2H56 and functional equivalents thereof. The amino acid sequence of Y2H56, the nucleotide sequence encoding Y2H56, and other related protein and nucleic acid molecules are also provided.

8 Claims, 0 Drawing figures

Exemplary Claim Number: 1

BRIEF SUMMARY:

1 BACKGROUND OF THE INVENTION

2 Extracellular stimuli associated with immune responses, inflammatory responses, and apoptosis activate kinases through receptor mediated processes. Ashkenazi and Dixit, Science 281, 1305-1308 (1998). For example,

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inflammatory cytokines such as tumor necrosis factor .alpha. (TNF.alpha.) or interleukin-1 (IL-1), activate kinases which in turn activate NF-.kappa.B by phosphorylating inhibitory proteins known as I.kappa.Bs. Phosphorylation of I.kappa.Bs is a key regulatory step for NF-.kappa.B mediated processes. See, for example, Baeuerle and Henkel, *Annu. Rev. Immunol.* 12, 141-179 (1994); Baldwin, *Annu. Rev. Immunol.* 14, 649-683 (1996); Siebenlist et al., *Annu. Rev. Cell Biol.* 12, 405-455 (1994); and Verma et al, *Genes Dev.* 9, 2723-2735 (1995). The kinases that phosphorylate I.kappa.Bs are called I.kappa.B kinases (IKKs).

- 3 The determination and characterization of kinases involved in signaling pathways leading to, for example, immune, inflammatory, and apoptotic responses is important for understanding and controlling these processes. Recently, an I.kappa.B kinase, designated IKK.alpha. but also referred to as CHUK (conserved helix-loop-helix ubiquitous kinase), was identified in a yeast-two-hybrid screen with NIK as bait. Regnier et al., *Cell* 90, 373-383 (1997). IKK.alpha. was determined to be responsible for the major I.kappa.B kinase activity induced by TNF stimulation of HeLa cells. DiDonato et al., *Nature* 388, 548-554 (1997). The identification of IKK.alpha. as a cytoplasmic kinase which phosphorylates I.kappa.B family members at their physiologically relevant sites and targets them for proteasome-mediated degradation was a major breakthrough.
- 4 The IKK.alpha. gene encodes a 745 amino-acid polypeptide (having a molecular mass of approximately 85 kDa). Murine and human IKK.alpha. cDNA clones were found to be almost identical. Connelly and Marcu, *Cellular and Molecular Biology Research* 41, 537-549 (1995).
- 5 Another kinase, termed IKK.beta., homologous to IKK.alpha., has also been reported. Stancovski and Baltimore, *Cell* 91, 299-302 (1997); Woronicz et al., *Science* 278, 866-869 (1997); and Zandi et al., *Cell* 91, 243-252 (1997). IKK.alpha. and IKK.beta. have 52% overall similarity to each other and 65% identity in the kinase domain. Zandi et al., *Cell* 91, 243-252 (1997). An I.kappa.B kinase termed T2K has also been described in U.S. Pat. No. 5,776,717 to Cao.
- 6 The known I.kappa.B protein kinases generally phosphorylate I.kappa.Bs at specific serine residues. For example, they specifically phosphorylate serines 32 and 36 of I.kappa.B.alpha.. Phosphorylation of both sites is required to efficiently target I.kappa.B.alpha. for destruction in vivo. Moreover, activation of IKK.alpha. and IKK.beta. occurs in response to NF-.kappa.B activating agents and mutant IKK.alpha. and IKK.beta. that are catalytically inactive block NF-.kappa.B stimulation by cytokines. These results highlight the important role played by I.kappa.B protein kinases in NF-.kappa.B activation processes. See Stancovski and Baltimore, *Cell* 91, 299-302 (1997) for a recent discussion of I.kappa.B kinases.
- 7 IKK.alpha. and IKK.beta., have structural motifs characteristic of the IKK kinases. This includes an amino terminal serine-threonine kinase domain separated from a carboxyl proximal helix-loop-helix (H-L-H) domain by a leucine zipper domain. These structural characteristics are unlike other kinases, and the domains are thought to be involved in protein-protein interactions.
- 8 Numerous proteins are involved in the signaling pathways that lead to immune, inflammatory, and apoptotic responses. A complete elucidation of these processes requires the identification of additional proteins that are involved and a determination of the protein interactions.
- 9 The discovery of additional proteins involved in these processes is important for controlling immune, apoptotic, and inflammatory processes. Thus, there is a great need for the identification and characterization of additional proteins involved in IKK mediated cellular processes.

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10 SUMMARY OF THE INVENTION

11 The present invention provides an isolated IKK binding protein comprising the amino acid sequence set forth in SEQ ID NO:1 and functional equivalents thereof. Also included are isolated nucleic acid molecules that encode the IKK binding protein comprising the amino acid sequence set forth in SEQ ID NO:1 and its functional equivalents, methods of making the IKK binding proteins comprising expressing nucleic acid molecules encoding the proteins, and antibodies directed to the IKK binding proteins.

12 DETAILED DESCRIPTION OF THE INVENTION

13 The invention is directed to an IKK binding protein, designated Y2H56, and its functional equivalents. Y2H56 will hereinafter refer to the protein defined by SEQ ID NO:1, which is found in humans.

14 In this specification, functional equivalents are proteins or fragments that are substantially homologous to SEQ ID NO:1 and that specifically bind to an IKK protein, such as IKK.alpha. or IKK.beta.. The term IKK is used herein to refer to all kinases that phosphorylate any I.kappa.B and that have helix-loop-helix and leucine zipper domains. Y2H56 and its functional equivalents bind to the region of the IKK proteins made up of the contiguous helix-loop-helix and leucine zipper domains.

15 In order to determine whether the sequence of a first protein, or fragment thereof, is substantially homologous to the sequence of a second protein, such as Y2H56, or fragment thereof, the sequences are first aligned so as to optimize the percent of amino acid residues that are identical, or that are identical or equivalent, at corresponding positions. Gaps may be introduced in the sequences, if necessary, to achieve optimization.

16 Amino acids generally considered to be equivalent are indicated below in separate rows (a) through (e):

17 (a) Ala (A), Ser (S), Thr (T), Pro (P), Gly (G)

18 (b) Asn (N), Asp (D), Glu (E), Gln (Q)

19 (c) His (H), Arg (R), Lys (K)

20 (d) Met (M), Leu (L), Ile (I), Val (V)

21 (e) Phe (F), Tyr (Y), Trp (W)

22 The amino acid sequences of highly homologous proteins can usually be aligned by visual inspection. If visual inspection is insufficient, the proteins are aligned in accordance with any of the methods described by George, D. G. et al, in *Macromolecular Sequencing and Synthesis, Selected Methods and Applications*, pages 127-149, Alan R. Liss, Inc. (1988), such as the formula described at page 137 using a match score of 1, a mismatch score of 0, and a gap penalty of -1.

23 In a first embodiment, the sequence of a protein or fragment thereof is considered substantially homologous to the sequence of Y2H56 or a fragment thereof if the amino acid sequences, after alignment, are at least about 25% identical, preferably at least about 35% identical, more preferably at least about 50% identical, even more preferably at least about 65% identical, still more preferably at least about 75% identical, most preferably at least about 85% identical, and, ideally at least about 95% identical.

24 In a second embodiment, the sequence of a protein or fragment thereof is considered substantially homologous to the sequence of Y2H56 or a fragment thereof if the amino acid sequences, after alignment, are at least about 50%

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identical or equivalent, preferably at least about 65% identical or equivalent, most preferably at least about 85% identical or equivalent, and ideally at least about 95% identical or equivalent.

- 25 Functional equivalents include all modifications of the polypeptide set forth in SEQ ID NO:1. These modifications may be introduced deliberately, as by site-directed mutagenesis, or may be natural variations and mutations. Such modifications include substitutions, additions, and/or deletions in the protein sequences as long as substantial homology and specific binding to IKK proteins are maintained.
- 26 For example, functional equivalents include variant Y2H56 proteins that are expressed by naturally occurring alleles. Alleles are alternative forms of a gene that occupy a given locus of a chromosome within a species.
- 27 Functional equivalents of Y2H56 also include proteins from non-human mammalian species (species orthologs) as well as proteins expressed by alleles of such species orthologs. Non-human mammals include, for example, primates, pet animals such as dogs and cats, laboratory animals such as rats and mice, and farm animals such as horses, sheep, and cows.
- 28 The proteins of the invention that do not occur in nature are isolated. The term "isolated" as used herein, in the context of proteins, refers to a polypeptide which is unaccompanied by at least some of the material with which it is associated in its natural state. The isolated protein constitutes at least 0.5%, preferably at least 5%, more preferably at least 25% and still more preferably at least 50% by weight of the total protein in a given sample.
- 29 Most preferably the "isolated" protein is substantially free of other
- 30 proteins, lipids, carbohydrates or other materials with which it is naturally associated, and yields a single major band on a non-reducing polyacrylamide gel. Substantially free means that the protein is at least 75%, preferably at least 85%, more preferably at least 95% and most preferably at least 99% free of other proteins, lipids, carbohydrates or other materials with which it is naturally associated.
- 31 ~~The invention also provides novel and/or isolated nucleic acid molecules that encode SEQ ID NO:1 and the functional equivalents thereof. Nucleic acid molecules (nucleic acids) of the invention include deoxyribonucleic acid (DNA), complementary DNA (cDNA), and ribonucleic acid (RNA) sequences.~~
- 32 ~~For example, the invention includes an isolated nucleic acid molecule as set forth in either SEQ ID NO:2 or SEQ ID NO:3, isolated nucleic acid molecules that are substantially homologous with SEQ ID NO:2 or SEQ ID NO:3, isolated nucleic acid molecules that hybridize with SEQ ID NO:2 or SEQ ID NO:3 under stringent conditions, nucleic acid sequences that are degenerate as a result of the genetic code, and the complements and fragments thereof.~~
- 33 In order to determine whether the sequence of a first nucleic acid molecule, or fragment thereof, is substantially homologous to the sequence of a second nucleic acid molecule, such as SEQ ID NO:2, or fragment thereof, the sequences are first aligned so as to optimize the percent of nucleotides that are identical at corresponding positions. Gaps may be introduced in the sequences if necessary to achieve optimization.
- 34 The nucleic acid sequences of highly homologous nucleic acid molecules can usually be aligned by visual inspection. If visual inspection is insufficient, the nucleic acid molecules are aligned in accordance with any of the methods described by George, D. G. et al, in Macromolecular Sequencing and Synthesis, Selected Methods and Applications, pages 127-149, Alan R. Liss, Inc. (1988), such as the formula described at page 137 using a

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match score of 1, a mismatch score of 0, and a gap penalty of -1.

- 35 In the present specification, the sequence of a nucleic acid molecule or fragment thereof is considered substantially homologous to SEQ ID NO:2, or a fragment thereof, if the nucleic acid sequences, after alignment, are at least about 40% identical, preferably at least about 50% identical, more preferably at least about 60% identical, even more preferably at least about 70% identical, still more preferably at least about 80% identical, most preferably at least about 90% identical, and, ideally at least about 95% identical.
- 36 The invention also includes nucleic acid molecules that hybridize to SEQ ID NO:2 or SEQ ID NO:3, a fragment of SEQ ID NO:2, a complement of SEQ ID NO:2, or a complement of a fragment of SEQ ID NO:2 under stringent conditions. Also included in the invention are a preferred group of protein functional equivalents of SEQ ID NO:1 encoded by nucleic acid molecules that hybridize under stringent conditions to a sequence complementary to SEQ ID NO:2 or a fragment of SEQ ID NO:2.
- 37 The term "stringent conditions," as used herein, is equivalent to "high stringent conditions" and "high stringency." These terms are used interchangeably in the art.
- 38 Stringent conditions are defined in a number of ways. In one definition, stringent conditions are selected to be about 50.degree. C. lower than the thermal melting point ($T_{sub}m$) for a specific sequence at a defined ionic strength and pH. The $T_{sub}m$ is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched sequence. Typical stringent conditions are those in which the salt concentration is about 0.02 M at pH 7 and the temperature is at least about 60.degree. C. Further examples of stringent conditions can be found in U.S. Pat. No. 5,789,550 to Goeddel et al. (1998). The description of stringent conditions in U.S. Pat. No. 5,789,550 is herein incorporated by reference.
- 39 Stringent conditions, in the nucleic acid hybridization context, include a combination of conditions, such as the nature and concentration of salts and organic solvents, temperature, and other parameters that are typically known to control hybridization reactions. The combination of parameters is more important than the measure of any single parameter. See U.S. Pat. No. 5,786,210; Wetmur and Davidson, J. Mol. Biol. 31, 349-370 (1968). Generally, stringent conditions are obtained at higher temperatures and lower ionic strength. Control of hybridization conditions, and the relationships between hybridization conditions and degree of homology are understood by those skilled in the art. See, for example, Bej, A. K., Nucleic Acid Hybridizations: Principles and Strategies, in Dangler, C. A. ed, Nucleic Acid Analysis:
- 40 Principles and Bioapplications, Wiley-Liss, Inc., pp. 1-29 (1996); Adams et al., The Biochemistry of the Nucleic Acids, pp. 605-606, Chapman & Hall (1992); Sambrook J, Fritsch EF, and Maniatis T, Molecular Cloning. A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory, Cold Spring Harbor (1989).
- 41 Fragments of nucleic acid molecules of the invention include primers and probes which are useful as tools in molecular biology and biotechnology. The fragment may or may not encode a polypeptide that binds to IKK.alpha. or IKK.beta.. Even if the encoded polypeptide does not bind, the fragment can be used; for example, as a primer ("amplimer") to selectively amplify nucleic acid, such as genomic DNA or total RNA. Primers can also be used in nucleic acid amplification procedures such as the polymerase chain reaction (PCR), ligase chain reaction (LCR), repair chain reaction (RCR), PCR oligonucleotide ligation assay (PCR-OLA), and the like.

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- 42 Fragments of the nucleic acid molecules of the invention can also be oligonucleotides complementary to a target nucleic acid molecule, i.e., the fragment can be a probe. Such oligonucleotides can be DNA or RNA. Oligonucleotides useful as probes in hybridization studies, such as in situ hybridization, can also be constructed.
- 43 The length of the oligonucleotide probe is not critical, as long as it is capable of hybridizing to the target molecule. The oligonucleotide should contain at least 6 nucleotides, preferably at least 10 nucleotides, and more preferably, at least 15 nucleotides. There is no upper limit to the length of the oligonucleotide probes. Longer probes are more difficult to prepare and require longer hybridization times. Therefore, the probe should not be longer than necessary. Normally, the oligonucleotide probe will not contain more than 50 nucleotides, preferably not more than 40 nucleotides, and, more preferably, not more than 30 nucleotides.
- 44 Numerous methods for detectably labeling such probes with radioisotopes, fluorescent tags, enzymes, binding moieties (e.g., biotin), and the like are known, so that the probes of the invention can be adapted for easy detectability. Methods for making and using nucleic acid probes are understood by those skilled in the art. See, for example, Keller G H and Manak M M, DNA Probes, 2d ed., Macmillan Publishers Ltd., England (1991) and Hames B D and Higgins S J, eds., Gene Probes I and Gene Probes II, IRL Press, Oxford (1995).
- 45 The nucleic acid molecules may contain synthetic sequences that do not occur in nature and/or they are isolated. The term "isolated," as used herein, in the context of nucleic acids, includes nucleic acid molecules unaccompanied by at least some of the material with which they are associated in their natural state. The isolated nucleic acid may constitute at least 0.5%, preferably at least 5%, more preferably at least 25% and still more preferably at least 50% by weight of the total nucleic acid in a given sample.
- 46 Most preferably the "isolated" nucleic acid is substantially free of other nucleic acids, proteins, lipids, carbohydrates or other materials with which it is naturally associated. Substantially free means that the nucleic acid is at least 75%, preferably at least 85%, more preferably at least 95% and most preferably at least 99% free of other nucleic acids, proteins, lipids, carbohydrates or other materials with which it is naturally associated. The nucleic acid molecules of the invention can also be recombinant, meaning that they comprise a non-natural sequence or a natural sequence joined to nucleotide(s) other than those in which they are joined on the natural chromosome.
- 47 Y2H56 was shown, using yeast two-hybrid screens, to bind to the carboxyl terminal domain regions of IKK.alpha. and IKK.beta.. See example 1. Y2H56 specifically binds with the region of the IKK proteins made up of the contiguous helix-loop-helix and leucine zipper domains. The binding of the Y2H56 protein to the IKKs is stronger than the binding of IKK.alpha. to a natural substrate of IKK.alpha., viz. I.kappa.BP.beta.2.
- 48 The Y2H56 protein and the other IKK.alpha. binding proteins described in example 1 are useful for elucidating and controlling pathways leading to inflammation and apoptosis. These processes are mediated by receptors such as tumor necrosis factor (TNF) receptors. The IKK binding proteins can also be used to detect IKK complexes and modulate IKK activity in cells undergoing signalling by inflammatory mediators such as TNF.alpha. and Il-1.
- 49 The Y2H56 protein and its functional equivalents are also useful for identifying therapeutically active agents that modulate the binding or interaction of Y2H56 and either IKK.alpha. or IKK.beta.. Such agents can either prevent the formation of Y2H56/IKK complexes or prevent or inhibit the dissociation of Y2H56/IKK complexes. Molecules that prevent the

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formation of Y2H56/IKK complexes or inhibit the dissociation of these complexes are useful for boosting the immune system, or as immunosuppressants, or as antiinflammatory agents.

- 50 Complex formation or dissociation can be determined by methods well known in the art. Such methods include, for example, gel filtration, sucrose density gradient centrifugation, crosslinking, and immunoprecipitation.
- 51 The proteins and variants of the proteins can be prepared by methods known in the art. Such methods include isolating the protein directly from cells, and synthesizing the protein chemically from individual amino acids. Preferably, the proteins of the invention can be prepared by providing DNA that encodes the protein, amplifying or cloning the DNA, expressing the DNA in a suitable host, and harvesting the protein.
- 52 DNA encoding the proteins of the invention can be synthesized or isolated. The DNA of the invention can be synthesized chemically from the four nucleotides in whole or in part by methods known in the art. Such methods include those described by Caruthers, Science 230, 281-285 (1985). DNA can also be synthesized by preparing overlapping double-stranded oligonucleotides, filling in the gaps, and ligating the ends together. See, generally, Sambrook et al. (1989) and Glover D M and Hames B D, eds., DNA Cloning, 2d ed., Vols. 1-4, IRL Press, Oxford (1995).
- 53 DNA expressing functional homologs of the protein can be prepared from wild-type DNA by site-directed mutagenesis. See, for example, Zoller and Smith, Nucleic Acids Res 10, 6487-6500 (1982); Zoller, Methods Enzymol 100, 468-500 (1983); Zoller, DNA 3(6), 479-488 (1984); and McPherson, ed., Directed Mutagenesis: A Practical Approach, IRL Press, Oxford (1991).
- 54 DNA encoding the protein of the invention can be isolated from different species by using the human sequence, SEQ ID NO:2, to prepare one or more oligonucleotide probes. The probe is labeled and used to screen a genomic or cDNA library in a suitable vector, such as phage lambda. The homology between the DNA of the Y2H56 of the species being screened and that of the human DNA is taken into account in determining the conditions of hybridization. The cDNA library may be prepared from mRNA by known methods, such as those described in Gubler and Hoffman, Gene 25, 263-270 (1983). Oligonucleotide probes can be used to screen cDNA libraries from different species and tissues. The oligonucleotide probe should be labeled so that it can be detected upon hybridization to DNA in the library being screened. These methods are well known in the art.
- 55 The DNA isolated is sequenced, and the sequence used to prepare additional oligonucleotide probes. This procedure may be repeated to obtain overlapping fragments until a complete open reading frame is produced.
- 56 The nucleic acids of the invention may be amplified by methods known in the art. One suitable method is the polymerase chain reaction (PCR) method described by Saiki et al., Science 239, 487 (1988), Mullis et al in U.S. Pat. No. 4,683,195 and by Sambrook et al. (1989). It is convenient to amplify the clones in the lambda-gt10 or lambda-gt11 vectors using lambda-gt10 or lambda-gt11-specific oligomers as the amplimers (available from Clontech, Palo Alto, Calif.). Other amplification procedures that are well known in the art such as ligase chain reaction (LCR), repair chain reaction (RCR), and PCR oligonucleotide ligation assay (PCR-OLA) can also be used to amplify the nucleic acids of the invention.
- 57 DNA encoding the proteins of the invention, or unique fragments thereof, may also be cloned in a suitable host cell and expressed by methods well known in the art. The DNA and protein may be recovered from the host cell. See, generally, Sambrook et al. (1989), for methods relating to the manufacture and manipulation of nucleic acids. The entire gene or additional fragments of the gene can be isolated by using the known DNA sequence or a fragment

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thereof as a probe. To do so, restriction fragments from a genomic or cDNA library may be identified by Southern hybridization using labeled oligonucleotide probes derived from SEQ ID NO:2.

- 58 The amplified or cloned DNA can be expressed in a suitable expression vector by methods known in the art. See, generally, Sambrook et al. (1989).
- 59 A variety of expression vectors and host cell systems can be used. These include, for example, microorganisms such as bacteria transformed with recombinant bacteriophage DNA, plasmid DNA, or cosmid DNA containing the Y2H56 coding region. Other expression vectors and host cell systems that can be used include yeast transformed with recombinant yeast expression vectors containing the Y2H56 coding sequence, insect cells infected with recombinant virus expression vectors containing the Y2H56 coding sequence, plant cells infected with recombinant virus expression vectors containing the Y2H56 coding sequence, or animal cells infected with recombinant virus expression vectors (e.g., retroviruses, adenovirus, vaccinia virus) containing the Y2H56 coding sequence.
- 60 The expression vectors useful in the present invention contain at least one expression control sequence that is operatively linked to the DNA sequence or fragment to be expressed. The control sequence is inserted in the vector in order to control and to regulate the expression of the cloned DNA sequence. Examples of useful expression control sequences are the lac system, the trp system, the tac system, the trc system, major operator and promoter regions of phage lambda, the control region of fd coat protein, the glycolytic promoters of yeast, e.g., the promoter for 3-phosphoglycerate kinase, the promoters of yeast acid phosphatase, e.g., Pho5, the promoters of the yeast alpha-mating factors, and promoters derived from polyoma, adenovirus, retrovirus, and simian virus, e.g., the early and late promoters or SV40, and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells and their viruses or combinations thereof.
- 61 Useful expression hosts include well-known prokaryotic and eukaryotic cells. Some suitable prokaryotic hosts include, for example, *E. coli*, such as *E. coli* SG-936, *E. coli* HB 101, *E. coli* W3110, *E. coli* X1776, *E. coli* X2282, *E. coli* DHI, and *E. coli* MRC1, *Pseudomonas* sp., *Bacillus* sp., such as *B. subtilis*, and *Streptomyces* sp. Suitable eukaryotic cells include yeasts and other fungi, insect, animal cells, such as COS cells and CHO cells, human cells and plant cells in tissue culture.
- 62 Preferably, Y2H56 is expressed using baculoviral vectors in insect cell cultures. In general, the transformation of insect cells and production of foreign proteins therein is disclosed in Guarino et al., U.S. Pat. No. 5,162,222.
- 63 Proteins can be isolated from a solubilized fraction by standard methods. Some suitable methods include precipitation and liquid chromatographic protocols such as ion exchange, hydrophobic interaction, and gel filtration. See, for example, *Methods Enzymol* (Guide to Protein Chemistry, Deutscher, ed., Section VII) pp. 182:309 (1990) and *Scopes, Protein Purification*, Springer-Verlag, New York (1987), which are herein incorporated by reference.
- 64 Alternatively, purified material is obtained by separating the protein on
- 65 preparative SDS-PAGE gels, slicing out the band of interest and electroeluting the protein from the polyacrylamide matrix by methods known in the art. The detergent SDS is removed from the protein by known methods, such as by dialysis or the use of a suitable column, such as the Extracti-Gel column from Pierce. Mixtures of proteins can be separated by, for example, SDS-PAGE in accordance with the method of Laemmli, *Nature* 227, 680-685 (1970). Such methods are well known in the art.

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- 66 The proteins of the invention can also be chemically synthesized by methods known in the art. Suitable methods for synthesizing proteins are described by Stuart and Young, *Solid Phase Peptide Synthesis*, 2d ed., Pierce Chemical Company (1984).
- 67 The invention also includes antibodies or antibody fragments that specifically bind to epitopes of the proteins of the invention defined by the amino acid sequence set forth in SEQ ID NO:1. An "antibody" in accordance with the present specification is defined broadly as a protein that binds specifically to an epitope. The antibodies of the invention can be monoclonal antibodies, polyclonal antibodies, chimerized antibodies, humanized antibodies, single chain antibodies, or a fragment thereof. For use in in vivo applications with human subjects, the antibody is preferably chimerized or humanized, containing an antigen binding region from, e.g., a rodent, with the bulk of the antibody replaced with sequences derived from human immunoglobulin.
- 68 Antibodies further include recombinant polyclonal or monoclonal Fab fragments prepared in accordance with the method of Huse et al., *Science* 246, 1275-1281 (1989).
- 69 Polyclonal antibodies are isolated from mammals that have been inoculated with the protein or a functional analog in accordance with methods known in the art. Briefly, polyclonal antibodies may be produced by injecting a host mammal, such as a rabbit, mouse, rat, or goat, with the protein or a fragment thereof capable of producing antibodies that distinguish between mutant and wild-type protein. The peptide or peptide fragment injected may contain the wild-type sequence or the mutant sequence. Sera from the mammal are extracted and screened to obtain polyclonal antibodies that are specific to the peptide or peptide fragment.
- 70 The antibodies are preferably monoclonal. Monoclonal antibodies may be produced by methods known in the art. These methods include the immunological method described by Kohler and Milstein, *Nature* 256:495-497 (1975) and by Campbell, in Burdon et al., eds, *Laboratory Techniques in Biochemistry and Molecular Biology*, Vol. 13, Elsevier Science Publishers, Amsterdam (1985); as well as the recombinant DNA method described by Huse et al. (1989).
- 71 To produce monoclonal antibodies, a host mammal is inoculated with a peptide or peptide fragment as described above, and then boosted. Spleens are collected from inoculated mammals a few days after the final boost. Cell suspensions from the spleens are fused with a tumor cell in accordance with the general method described by Kohler and Milstein (1975). See also Campbell (1985). To be useful, a peptide fragment must contain sufficient amino acid residues to define the epitope of the molecule being detected.
- 72 If the fragment is too short to be immunogenic, it may be conjugated to a carrier molecule. Some suitable carrier molecules include keyhole limpet hemocyanin and bovine serum albumin. Conjugation may be carried out by methods known in the art. One such method is to combine a cysteine residue of the fragment with a cysteine residue on the carrier molecule.
- 73 Methods for making chimeric and humanized antibodies are also known in the art. For example, antibodies can be engineered using genetic techniques to produce chimeric antibodies including protein components from two or more species.
- 74 For example, methods for making chimeric antibodies include those described in U.S. patents by Boss (Celltech) and by Cabilly (Genentech). See U.S. Pat. Nos. 4,816,397 and 4,816,567, respectively. Methods for making humanized antibodies are described, for example, in Winter, U.S. Pat. No. 5,225,539, Co et al., *Nature* 351, 501-502 (1992); Queen et al., *Proc. Natl. Acad. Sci.*

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86, 10029-1003 (1989) and Rodrigues et al., Int. J. Cancer, Supplement 7, 45-50 (1992).

- 75 Methods are also known for inducing expression of engineered antibodies in various cell types, such as mammalian and microbial cell types. Numerous techniques for preparing engineered antibodies are described, for example, in Owens and Young, "The genetic engineering of monoclonal antibodies," J. Immunol. Meth. 168, 149-165 (1994).
- 76 Methods for making single chain antibodies are also known in the art. Some suitable examples include those described by Wells et al. in European patent application 502 812 and Int. J. Cancer 60, 137-144 (1995).
- 77 Assays for directly detecting the presence of Y2H56 and its functional equivalents with antibodies follow known formats, such as, fluorescent activated flow cytometry, fluorescent microscopy, and immuno-electron microscopy. Moreover, assays for detecting the presence of proteins with antibodies have been previously described and follow known formats, such as standard blot and ELISA formats. These formats are normally based on incubating an antibody with a sample suspected of containing the protein and detecting the presence of a complex between the antibody and the protein. The antibody is labeled either before, during, or after the incubation step. The protein is preferably immobilized prior to detection. Immobilization may be accomplished by directly binding the protein to a solid surface, such as a microtiter well, or by binding the protein to immobilized antibodies.
- 78 Suitable assays are known in the art, such as the standard ELISA protocol described by R. H. Kenneth, "Enzyme-linked antibody assay with cells attached to polyvinyl chloride plates" in Kenneth et al., Monoclonal Antibodies, Plenum Press, New York, pp. 376 et seq. (1981).

DETAILED DESCRIPTION:

1 EXAMPLES

2 Example 1

3 Y2H56 Binds IKKs

4 ~~A yeast two hybrid screen was undertaken with IKK.alpha. as a bait in an attempt to identify interacting proteins which could represent in vivo regulators of the cytokine induced kinase cascade.~~ Full length IKK.alpha. and smaller fragments in the Field's pGTB9c bait vector (see Fields and Sternglanz, Trends Genet. 10, 286-292 (1994)) met with technical problems owing to its inherent in vivo transactivation properties. These problems were overcome by incorporating a high dose of an inhibitor of the product of the His3 selection gene thereby severely restricting yeast colony growth. (Triazole or 3-AT (3-amino-1, 2, 4-triazole or aminotriazole) has been reported to competitively inhibit the product of the yeast His3 gene in a dose dependent manner (Klopotoski et al., Arch. Biochem. Biophys. 112, 562-566 (1965)). The bait vector's insert was a 937 bp SnaB1/XhoI fragment of the murine IKK.alpha. clone encoding the protein's leucine zipper, helix-loop-helix and carboxyl terminus. The latter bait vector was transfected into the Y153 yeast strain and a colony that grew on agar without tryptophan was selected for further transfections according to standard protocols (Yeast Matchmaker manual, Clontech Inc., Palo Alto, Calif.). Yeast harboring the bait grew on histidine-minus plates. However, this non-specific growth was abrogated by the inclusion of 50 .mu.M (3-AT) that would also yield the strongest interactors. Y153 cells harboring the bait vector were transfected with a B lymphoblast cDNA library (0.6.times.10.sup.9 cfu, ATCC #87003) (Durfee et al., Genes Dev 7, 555-569 (1993)) sub-cloned into plasmid BNN132 (for a final transfection frequency

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of 10.sup.5 clones), which were spread onto 30 agar plates (His-, Trp-, Leu-, 50 mM 3-AT). 126 clones showing a faster growth rate compared to background colonies were picked after 3 and 6 days incubation at 30.degree. C. and replated. 70 clones were selected for plasmid isolation based on their growth on His-, Trp-, Leu-, 50 .mu.M 3-AT plates. From these 70 picks secondary picks, 16 clones remained positive after multiple rounds of purification and rescreening (14 of these sixteen were unique and two were isolated twice).

TABLE 1

Results of a Yeast Two-Hybrid Screen with IKK.alpha. Helix-Loop-Helix and Leucine Zipper Domains as Bait

Relative Interaction		Insert	
Y2h Clones	Strength	Length	Identity
11	+	0.8 kB	RanBP5
52.sup.#	++	0.9 kB	CoA Reductase
21	++	1.3 kB	TRIP9/HuI.kappa.B.beta.2
29.sup.#	++	1.1 kB	HuTCP-1
31	++	1.5 kB	Hsp40
37	+	2.3 kB	BS4 (Interferon Induced Protein)
67	+	1.5 kB	Phospholipase A2
71	+	0.8 kB	Calmodulin
70	+	1.5 kB	HuSgn3
14*	++	1.2 kB	HuAD3 Locus
35*	+++	1.2 kB	Cosmid near Btk
56*	+++	0.9 kB	p33ING1-like
53*	+++	1.2 kB	Unknown
61**	+	0.7 kB	Unknown

Legend:

Fourteen yeast two hybrid clones obtained from a human B lymphoblastoid cell cDNA library which specifically interact with the contiguous helixloop-helix and leucine zipper domains of the IKK.alpha. protein. M clones (Y2h11,21,29, 70,14,35,56 and 53) also bound to an analogous IKK.beta. bait with similar or even greater strength except for Hsp40 which only specifically bound to the IKK.alpha. bait. All clones reproducibly failed to significantly interact with an empty bait vector and #two other bait vectors harboring either the IKK.alpha. Leucine Zipper or HelixLoop-Helix domains. The relative interaction strengths are based on the growth rates (i.e., colony size) of each clone.

.sup.# Isolated Twice;

*Unknown strong interacting proteins;

**Unknown weak interacting protein.

- 5 The fourteen clones are shown in Table 1. These results demonstrate the presence of a family of IKK.alpha. binding proteins. Nine of the 14 clones are known proteins and the remaining five specify novel proteins: three of which interact with the bait more strongly than IKK.alpha.'s I.kappa.B.beta. substrate (Y2h35, 53 and 56), one in a comparable fashion to I.kappa.B.beta. (Y2h14) and one exhibited weaker binding (Y2h61). Several of the known proteins are involved in either signaling and/or molecular trafficking pathways in cells. RanBP5 was isolated as a Ran binding protein and Ran is a small GTP-binding and- hydrolyzing protein predominantly located in the nucleus (Deane et al., Mol. Cell Biol. 17, 5087-5096 (1998). RanBP5 is related to importin-.beta., a mediator of nuclear localization signal (NLS)-dependent nuclear transport. TRIP9/HuI.kappa.B.beta.2 is the predominant isoform of I.kappa.B.beta. in human cells and a known physiological substrate of the IKK.alpha. kinase (Lee et al., Mol.

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Endocrinol. 9, 243-254 (1995); Hirano et al., Mol. Cell. Biol. 18, 2596-2607 (1998)). The presence of I.kappa.B.beta. amongst these IKK.alpha. interacting proteins validates the specificity of the screen and also demonstrates the I.kappa.Bs do not require the IKK.alpha. amino terminal kinase domain for binding. Hsp40 and TCP-1 are chaperone proteins which might bind to the bait due to a partially unfolded conformation (in the context of a Gal4dbd chimera). A database of frequently isolated clones in yeast two hybrid screens does contain several hsp proteins but Hsp40 and TCP1 are not represented amongst these frequently isolated, presumably false positive genes. Alternatively, they may also be natural interactors of IKK.alpha. that might be involved in its in vivo cytoplasmic trafficking. HuSgn3 was recently described as a component of a 450 kDa protein complex that also possesses an I.kappa.B kinase activity. Seeger et al., FASEB J. 12, 469-478 (1998). Sgn3 also exhibited sequence similarities to regulatory components of the 26S proteasome complex. Calmodulin is the principal calcium sensor in the cell, which when complexed to two calcium ions, acts as a regulator for a variety of intracellular enzymes including kinases such as CaM-kinase II, the serine/threonine specific phosphatase, Calcineurin and proteins which maintain the cytoskeletal architecture.

- 6 Y2H56 is highly homologous with the p33-ING1 tumor suppressor protein having about 45% identity and about 70% overall similarity. The p33-ING1 tumor suppressor protein has been shown to functionally interact with the p53 tumor suppressor protein to arrest cellular growth and induce apoptosis. Garkavtsev et al., Nature Genetics 14, 415-420 (1996).

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CLAIMS:

What is claimed is:

1. An isolated nucleic acid molecule comprising a sequence that encodes an IKK binding protein having SEQ ID NO:1 or its allelic variants.
2. An isolated nucleic acid molecule according to claim 1 comprising SEQ ID NO:2, SEQ ID NO:3, or sequences that have at least 85% identity thereto.
3. An isolated nucleic acid molecule according to claim 1 comprising SEQ ID NO:2 or SEQ ID NO:3.
4. An isolated nucleic acid molecule encoding an IKK binding protein that hybridizes under stringent conditions to a nucleic acid molecule selected from the group consisting of SEQ ID NO:2, and SEQ ID NO:3.
5. An isolated nucleic acid molecule fully complementary to the nucleic acid molecule of either SEQ ID NO:2 or SEQ ID NO:3.
6. A method of making an IKK binding protein or its allelic variants, comprising:

incorporating into a host cell a nucleic acid molecule that encodes an IKK binding protein comprising a sequence as set forth as SEQ ID NO:1 or its allelic variants;

expressing the nucleic acid molecule; and

isolating the IKK binding protein or its allelic variants.
7. A method according to claim 6, wherein the nucleic acid molecule that encodes an IKK binding protein comprising a sequence set forth as SEQ ID NO:1 or its allelic variants comprises either SEQ ID NO:2 or SEQ ID NO:3.
8. A method of making an IKK binding protein, comprising:

incorporating into a host cell a nucleic acid molecule that encodes an IKK binding protein wherein the nucleic acid molecule that encodes an IKK binding protein or its allelic variants comprises a nucleic acid molecule that is at least 85% identical to either the nucleic acid molecule of SEQ ID NO:2 or SEQ ID NO:3.

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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FEATURES
source

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Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
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Note: this is a NIH_MGC library."

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Db 840 GTTCGGTGTACTACTAGTAAC 860

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RESULT 2
BO679158      995 bp      mRNA      linear      EST 15-JUL-2002
BO679158      AGENCOURT_8034407 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6213872
LOCUS
DEFINITION
5', mRNA sequence.
ACCESSION
BO679158.1 GI:21791837
VERSION
BO679158.1
KEYWORDS
SOURCE
HUMAN
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE
1 (bases 1 to 995)
NIH-MGC http://mgi.mcl.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgraphs-remail.nih.gov
COMMENT
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2380 row: e column: 09
High quality sequence stop: 638.
Location/Qualifiers

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FEATURES
source
1..995
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6213872"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: skin; Vector: pORF7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."

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BASE COUNT      268 a      260 c      287 g      180 t
ORIGIN

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Query Match      77.8%; Score 745; DB 14; Length 995;
Best Local Similarity 98.0%; Pred. No. 8.6e-179;
Matches 765; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

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OY 156 CTGATAGTATCGAAGACCTCCCTCGAAGCTTCAGAGAACTTCAGCTGATGCGAG 215
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Db 46 CTGACAGATATCGAAGACCTCCCTCGAAGCTTCAGAGAACTTCAGCTGATGCGAG 105

OY 216 CTGGACCCAGAGAGAGAGATAAGAAAGCAGAGATTGACATCTGCTGCGAGATCATC 275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 106 CTGGACCCAGAGAGAGAGATAAGAAAGCAGAGATTGACATCTGCTGCGAGATCATC 165

OY 276 TTCACGGTGAAGAGCGCTGTCTCCAGACACGCGGTGAGCGCTGCAGAAATCCAGAAC 335
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Db 166 TTCACGGTGAAGAGCGCTGTCTCCAGACACGCGGTGAGCGCTGCAGAAATCCAGAAC 225

OY 336 GCCTACAGCAAGTGAAGAAATACAGTGAAGACAAATGCGAGTGGCATCGACCTAC 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 GCCTACAGCAAGTGAAGAAATACAGTGAAGACAAATGCGAGTGGCATCGACCTAC 285

OY 396 GAGATGGTGAATTAACACATTCGAAAGCTTGATGCGAGACCTGGCGGCTTTGAAGCAGAT 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 286 GAGATGATGATAAACAATTCGAAAGGCTTGATGACGACATGCGCGCTTTGAACGACAT 345
Qy 456 CTGAAGGCAAGATGAGAGGCAATGATTTTGAAGCTCCGAGGCGGAGGTTAAAAAA 515
Db 346 CTGAAGGCAAGATGAGAGGCAATGATTTTGAAGCTCCGAGGCGGAGGTTAAAAAA 405
Qy 516 GGCCGGGCTCAGAAAAAGAGGCTCCGAGGCGGAGGCAATGACAGAGAA 575
Db 406 GGCCGGGCTCAGAAAAAGAGGCTCCGAGGCGGAGGCAATGACAGAGAA 465
Qy 576 GACACACCAAGAAAAAGAGGCAATGAGAGGCTGATGATTCACAGACATCCTGTC 635
Db 466 GACACACCAAGAAAAAGAGGCAATGAGAGGCTGATGATTCACAGACATCCTGTC 525
Qy 636 GTGACACCCCTGATGATGCTGACATGCTGACATGCTGACATGCTGACATGCTG 695
Db 526 GTGACACCCCTGATGATGCTGACATGCTGACATGCTGACATGCTGACATGCTG 585
Qy 696 TGCCACACGATCTCTATGAGGAGATGATGAGGCTGATGATTCACAGACATCCTGTC 755
Db 586 TGCCACACGATCTCTATGAGGAGATGATGAGGCTGATGATTCACAGACATCCTGTC 645
Qy 756 TGGTTTCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 815
Db 646 TGGTTTCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705
Qy 816 CGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 874
Db 706 CGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Qy 875 AGCAAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 934
Db 766 GAGCAGGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 825
Qy 935 T 935
Db 826 T 826

RESULT 3
B0686855
LOCUS
DEFINITION B0686855 904 bp mRNA linear EST 15-JUL-2002
5', mRNA sequence. IMAGE:6248487
ACCESSION B0686855
VERSION B0686855.1 GI:21812171
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at:
<http://image.llnl.gov>
Plate: LCM238 row: 9 column: 16
High quality sequence stop: 664.
Location/Qualifiers
1. 904
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6248487"
/clone_id="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
BASE COUNT 252 a 215 c 265 g 170 t 2 others
ORIGIN
Query Match 76.8%; Score 735.8; DB 14; Length 904;
Best Local Similarity 97.8%; Pred. No. 1.9e-176;
Matches 787; Conservative 0; Mismatches 14; Indels 4; Gaps 4;
Qy 156 CTGATAGTATCGAGAACCTTCCCTGCAACTTCAGAGAACTTCACAGTATGAGAG 215
Db 60 CTGAGACATATGAGAACCTTCCCTGCAACTTCAGAGAACTTCACAGTATGAGAG 119
Qy 216 CTGACACAGAGAGCGGAGATAGAGACAGAGATTCATCTGCTGCTGACAGTATC 275
Db 120 CTGACACAGAGAGCGGAGATAGAGACAGAGATTCATCTGCTGCTGACAGTATC 179
Qy 276 TCACAGGAGAGAGCGCTGCTCCAGACAGCGCGTGGAGCGCTGACAGATCCAGAAC 335
Db 180 TCACAGGAGAGAGCGCTGCTCCAGACAGCGCGTGGAGCGCTGACAGATCCAGAAC 239
Qy 336 GCTTACACAGAGTGCAGAGATACAGTACAGTACAGTACAGTACAGTACAGTACAG 395
Db 240 GCTTACACAGAGTGCAGAGATACAGTACAGTACAGTACAGTACAGTACAGTACAG 299
Qy 396 GAGATGATGATTAACACATTCGAGAGCTTGATGACAGCTGCGCGCTTTGAAGCAGAT 455
Db 300 GAGATGATGATTAACACATTCGAGAGCTTGATGACAGCTGCGCGCTTTGAAGCAGAT 359
Qy 456 CTGAAGGCAAGATGAGAGGCAATGATTTGAAGCTCCGAGGCGGAGGTTAAAAAA 515
Db 360 CTGAAGGCAAGATGAGAGGCAATGATTTGAAGCTCCGAGGCGGAGGTTAAAAAA 419
Qy 516 GGCCGGGCTCAGAAAAAGAGGCTCCGAGGCGGAGGCAATGACAGAGAA 575
Db 420 GGCCGGGCTCAGAAAAAGAGGCTCCGAGGCGGAGGCAATGACAGAGAA 479
Qy 576 GACACACCAAGAAAAAGAGGCAATGAGAGGCTGATGATTCACAGACATCCTGTC 635
Db 480 GACACACCAAGAAAAAGAGGCAATGAGAGGCTGATGATTCACAGACATCCTGTC 539
Qy 636 GTGACACCCCTGATGATGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695
Db 540 GTGACACCCCTGATGATGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
Qy 696 TGCCACACGATCTCTATGAGGAGATGATGAGGCTGATGATTCACAGACATCCTGTC 755
Db 600 TGCCACACGATCTCTATGAGGAGATGATGAGGCTGATGATTCACAGACATCCTGTC 659
Qy 756 TGGTTTCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 815
Db 660 TGGTTTCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719
Qy 816 CGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873
Db 720 CGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779
Qy 874 GAGCAAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 932
Db 780 GAGCAAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 839
Qy 933 CTGCTTC-GGTTGATCTTATGATAC 956
Db 840 CTGCTTCGGGTTGATCTTAAAAAC 864

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BO687622	AGENCOURT_8171406 NIH_MGC_110 Homo sapiens cDNA clone IMAGE7051931	BO687622	BO687622.1	GI:21812938	human.	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
AUTHORS	1 (bases 1 to 879)					
TITLE	NIH-MGC http://mgc.nci.nih.gov/					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory DNA Sequencing by: The I.M.A.G.E. Consortium (LNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LNCM2397 row: g column: 04 High quality sequence stop: 645. Location/Qualifiers 1..879 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6251931" /clone_id="NH_MGC_110" /tissue_type="ductal carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: pancreas; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-GDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."					
FEATURES						
source						
BASE COUNT	245 a 210 c 256 g 168 t					
ORIGIN						
Query Match	Best Local Similarity 75.5%; Score 723; DB 14; Length 879;					
Matches 773:	Conservative 0; Mismatches 10; Indels 4; Gaps 4;					
OY	156 CTGATAGGTATTCGAGAACCTTCCCTCGCACTTCAGAGAACTTCACGTATGGCAGAG 215					
DB	40 CTGCACACTATTTCGAGAACCTTCCCTCGCACTTCAGAGAACTTCACGTATGGCAGAG 99					
OY	216 CTGCACAGAGAGAGCGAAGATTAAGAAGACAGATTTGATCTCCGCGTGACAGATCATC 275					
DB	100 CTGCACAGAGAGCGAAGATTAAGAAGACAGATTTGATCTCCGCGTGACAGATCATC 159					
OY	276 TCACAGGTGAAGACGCTGTCTCCAGACCAGCGCGGTGAGGCCCTGCAGAGAATCCAGAAC 335					
DB	160 TCACAGGTGAAGACGCTGTCTCCAGACCAGCGCGGTGAGGCCCTGCAGAGAATCCAGAAC 219					
OY	336 GCCTACACAGAGTGCGAAGATPACAGTAGACAGCAAAGTGACGTGGCCATCGACACTAC 395					
DB	220 GCCTACACAGAGTGCGAAGATPACAGTAGACAGCAAAGTGACGTGGCCATCGACACTAC 279					
OY	396 GAGATGGTGGAATAACAATTCGAAAGCGTTGATCGAGACCTGGCGCGCTTTGAAGCAAT 455					
DB	280 GAGATGGTGGAATAACAATTCGAAAGCGTTGATCGAGACCTGGCGCGCTTTGAAGCAAT 339					
OY	456 CTGAAGGCAAGATGAGAGCGAGTGATTTTAAAGCTCCGAGGGCGAGGGTTAAAAAAA 515					
DB	340 CTGAAGGCAAGATGAGAGCGAGTGATTTTAAAGCTCCGAGGGCGAGGGTTAAAAAAA 399					

QY	516	GGCCGGGGTCTGAAAGAAAAAGAGGCTCCCGGGCCGAGCGAGAGAGCATCAGAGAA	575
Db	400	GGCCGGGGTCTGAAAGAAAAAGAGGCTCCCGGGCCGAGCGAGAGAGCATCAGAGAA	459
QY	576	GACACACCAAGAAAAAGAGCACAAAGAGGGTCTGAGTTCACTGACACCATCTGTCC	635
Db	460	GACACACCAAGAAAAAGAGCACAAAGAGGGTCTGAGTTCACTGACACCATCTGTCC	519
QY	636	GTGACCCCTCTGATGTAGTGGAGCATGCCGTGGACCCAAAGCAACCATCTGCTG	695
Db	520	GTGACCCCTCTGATGTAGTGGAGCATGCCGTGGACCCAAAGCAACCATCTGCTG	579
QY	696	TGCACACGAGCTCTCTATGGGAGATGATTGGCTGTGACAAATCCAGACTGTCCATTGAG	755
Db	580	TGCACACGAGCTCTCTATGGGAGATGATTGGCTGTGACAAATCCAGACTGTCCATTGAG	639
QY	756	TGCTTTACCTTGGCTCGCT - GGAACCTTACCAGAAACCAAGGAAATGGTCTGTCC	814
Db	640	TGCTTTACCTTGGCTCGCTGTGGACCTTACCAGAAACCAAGGAAATGGTCTGTCC	699
QY	815	ACGCTGTGTCAGAGAAAAAG - GGAAGAAGAATGAGAGAGACTGTGTGCCCGATCGA -	872
Db	700	ACGCTGTGTCAGAGAAAAAGGAGGAAGAAGAATGAGAGAGACTGTGTGCCCGATCGAG	759
QY	873	GGAGCAAGTTAATCTGTCCC - TTCATTGCTGTGCAATATTTCCTCTCTTTAAAACTA	931
Db	760	GGAGCAAGTTAATCTGTCCCCTTCTTCGTGTGCAATATTTCCTCTTTAAAACTA	819
QY	932	CCCTGTT 938	
Db	820	CCTTGCT 826	

FEATURES	source
LOCUS	BO877416
DEFINITION	BO877416 941 bp mRNA linear EST 16-Aug-2002
ACCESSION	AGNCOURT_8071188 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6090578
VERSION	5, mRNA sequence.
KEYWORDS	BO877416 BO877416.1 GI:22269424
ORGANISM	EST. human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL	1 (bases 1 to 941)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaps@email.nih.gov Tissue Procurement: DCTD/DTF CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov plate: LCM2332 row: d column: 03 High quality sequence stop: 556. Location/Qualifiers 1. 941 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6090578" /clone_id="NIH_MGC_112" /tissue_type="melanotic melanoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pOT87; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGACGGG(6). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library.
BASE COUNT 262 a 238 c 266 g 175 t
ORIGIN

Query Match 74.6%; Score 714.6; DB 14; Length 941;
Best Local Similarity 98.3%; Pred. No. 4.6e-171;
Matches 764; Conservative 0; Mismatches 9; Indels 4; Gaps 4;
QY 156 CTGATAGTATGAGAACCTTCCCTGCGAATCTTCAGAGAACTTCACCTGATGCGAGAG 215
DB 46 CTGACAGATGAGAACCTTCCCTGCGAATCTTCAGAGAACTTCACCTGATGCGAGAG 105
QY 216 CTGACACGAGAGAGCGAAGATAGAAAGCAGATTGACATCTGGCTGCGAGATCATC 275
DB 106 CTGACACGAGAGAGCGAAGATAGAAAGCAGATTGACATCTGGCTGCGAGATCATC 165
QY 276 TCCACGGTGAAGAGCTGCTCCAGACAGCGCGTGGAGCGCTGCGAAGATCCAGAAC 335
DB 166 TCCACGGTGAAGAGCTGCTCCAGACAGCGCGTGGAGCGCTGCGAAGATCCAGAAC 225
QY 336 GCCTACAGCAAGTGCAGAGGAATATACAGTACGACAAAGTGCAGCTGGCATGCAAGCTAC 395
DB 226 GCCTACAGCAAGTGCAGAGGAATATACAGTACGACAAAGTGCAGCTGGCATGCAAGCTAC 285
QY 366 GAGATGTGATTAACACATTCGAAAGCTGTATGACAGACCTGGCGCTTTGAGCAGAT 455
DB 286 GAGATGTGATTAACACATTCGAAAGCTGTATGACAGACCTGGCGCTTTGAGCAGAT 345
QY 456 CTGAAGGACAAAGATGAGAGGCGATTTTGAAGCTCCGAGGCGAGAGGTTAAAGAA 515
DB 346 CTGAAGGACAAAGATGAGAGGCGATTTTGAAGCTCCGAGGCGAGAGGTTAAAGAA 405
QY 516 GGCCGGGGTTCAGAAAGAAAGAGGCTCCCGGGCCGAGGAGAGAGCATCAGAGAA 575
DB 406 GGCCGGGGTTCAGAAAGAAAGAGGCTCCCGGGCCGAGGAGAGAGCATCAGAGAA 465
QY 576 GACACACCAAGAAAGAAAGAGAGGCTGTGATTCAGTACGACCATCTCTCC 635
DB 466 GACACACCAAGAAAGAAAGAGAGGCTGTGATTCAGTACGACCATCTCTCC 525
QY 636 GTGCACCCCTGTGATGTGGACATGCCCGTGGACCCAAAGAACCCAGTACTGCCG 695
DB 526 GTGCACCCCTGTGATGTGGACATGCCCGTGGACCCAAAGAACCCAGTACTGCCG 585
QY 696 TGCCACAGAGTCTCTATGGGAGATGATGGCTGTGACAAATCCAGACTGTCCAATTGAG 755
DB 586 TGCCACAGAGTCTCTATGGGAGATGATGGCTGTGACAAATCCAGACTGTCCAATTGAG 645
QY 756 TGGTTTCACTTGGCTGGCTGGAGCTTACACAGAAACCCAAAGAAATGTTGTGTCCA 815
DB 646 TGGTTTCACTTGGCTGGCTGGAGCTTACACAGAAACCCAAAGAAATGTTGTGTCCA 705
QY 816 CGGTGTGTCACAG-AAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 873
DB 706 CGGTGTGTCACAGAAAG 765
QY 874 GAGCAAGTTAATCT-GTCCCTTCAATTCGT-GTGCATATTTTCCCTCTTTTAA 928
DB 766 GAGCAAGTTAATCTGTGCTCCCTCATTTGTCATATTTCCCTTTCTTTTAA 822

RESULT 6
LOCUS B0883988 989 bp mRNA linear EST 16-AUG-2002
DEFINITION AGNCORRT.8073788 NIH_MGC_110 Homo sapiens cDNA clone IMAGE6089499
ACCESSION B0883988
VERSION B0883988.1 GI:22275996
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 989)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: LINC2313 row: 1 column: 21
High quality sequence start: 21
High quality sequence stop: 589.
location/Qualifiers

FEATURES
source

1. 989
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/db_xref="taxon:9606"
/clone="IMAGE:6083492"
/clone_lib="NIH-MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."
BASE COUNT 260 a 257 c 288 g 184 t
ORIGIN

Query Match 74.2%; Score 711; DB 14; Length 989;
Best Local Similarity 95.3%; Pred. No. 3.8e-170;
Matches 765; Conservative 0; Mismatches 35; Indels 3; Gaps 3;

QY 156 CTGATAGTATGAGAACCTTCCCTGCGAATCTTCAGAGAACTTCACCTGATGCGAGAG 215
DB 69 CTGACAGATGAGAACCTTCCCTGCGAATCTTCAGAGAACTTCACCTGATGCGAGAG 128
QY 216 CTGACACGAGAGAGCGAAGATAGAAAGCAGATTGACATCTGGCTGCGAGATCATC 275
DB 129 CTGACACGAGAGAGCGAAGATAGAAAGCAGATTGACATCTGGCTGCGAGATCATC 188
QY 276 TCCACGGTGAAGAGCTGTCTCCAGACAGCGCTGGAGCGCTTCAGAAAGTCCAGAAC 335
DB 189 TCCACGGTGAAGAGCTGTCTCCAGACAGCGCTGGAGCGCTTCAGAAAGTCCAGAAC 248
QY 336 GCCTACAGCAAGTGCAGAGGAATATACAGTACGACAAAGTGCAGCTGGCATGAGACCTAC 395
DB 249 GCCTACAGCAAGTGCAGAGGAATATACAGTACGACAAAGTGCAGCTGGCATGAGACCTAC 308
QY 396 GAGATGTGATTAACACATTCGAAAGCTGTGATGACAGACTTCCGCGCTTTGAAGCAGAT 455
DB 309 GAGATGTGATTAACACATTCGAAAGCTGTGATGACAGACTTCCGCGCTTTGAAGCAGAT 368
QY 456 CTGAAGGACAAAGATGAGAGGCGATTTTGAAGCTCCGAGGCGAGAGGTTAAAGAA 515
DB 369 CTGAAGGACAAAGATGAGAGGCGATTTTGAAGCTCCGAGGCGAGAGGTTAAAGAA 428
QY 516 GGCCGGGGTTCAGAAAGAAAGAGGCTCCCGGGCCGAGGAGAGAGAGCATCAGAGAA 575
DB 429 GGCCGGGGTTCAGAAAGAAAGAGGCTCCCGGGCCGAGGAGAGAGCATCAGAGAA 488
QY 576 GACACACCAAGAAAGAAAGAGAGGCTGTGATTCAGTACGACCATCTCTGCC 635
DB 489 GACACACCAAGAAAGAAAGAGAGGCTGTGATTCAGTACGACCATCTCTGCC 548

OY	636	GTGCACCCCTCGATGCTGCTGGACATGGCCCGGAGACCCAAAGAACCCACGACTGACCTG	695
Db	549	GTGCACCCCTCGATGCTGCTGGACATGGCCCGGAGACCCAAAGAACCCACGACTGACCTG	608
OY	696	TGCCACACAGTCTCCTATGAGGAGATGATGATGGCTTGACCAATCCAGACTGTCCAAATTGAG	755
Db	609	TGCCACACAGTCTCCTATGAGGAGATGATGATGGCTTGACCAATCCAGACTGTCCAAATTGAG	668
OY	756	TGCTTTCACTTTGCCCTGCGTGGACCTTACACAGAAACCCAAAGAAAAATGGTTCTGTCCA	815
Db	669	TGCTTTCCCTTTGCTGCGTGGACCTTACACAAAAACC - AAGGAAATATGGTTCGTGCCA	727
OY	816	CGGTGTGTTCAGAGAAAGAGAGAGAAAGATG - GGAGAGCTGTGTG - CCGGATCCGAG	873
Db	728	CCGGGTGTGCCCCGGAAAAAGAGAGAAAGATGAGGAGGCTGTGTGCCCCCGGAGACCCGAG	787
OY	874	GAGCAAGTTAATCTGTCGCTTCATTCGCTCGTGTGCAATATTTCCCTCCCTTTAAACTACG	933
Db	788	GAGCAAGTTAATCTGCCCCCTTCTTTCGCGCCGCAATATTTCCCTCTTTTAAACTACG	847
OY	934	TTGTTCGGTTGATCTAGTATGTAAC	956
Db	848	TTGTTCGGGTGATCTAGTATGTAAC	870

RESULT 7					
B0688356					
LOCUS	B0688356	874 bp	mRNA	linear	EST 15-JUL-2002
DEFINITION	AGNCSCURT_8064337 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6207958 5' mRNA sequence.				

ACCESSION	BQ688356
VERSION	BQ688356.1
KEYWORDS	GI:21813672
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Euharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	1 (bases 1 to 874)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.

FEATURES

Email: c9apb5-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNU)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNU at:
<http://image.llnl.gov>
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High quality sequence stop: 649.
Location/Qualifiers

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/clone IMAGE:6207958"
/clone_11b="NH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH_MGC library"

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BASE COUNT	246 a	209 c	255 g	164 t
ORIGIN	NOTE: THIS IS A NMR/MSC LIBRARY.			
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Best Local Similarity 97.18; Pred. NO. 5.8e-165;
Matches 768; Conservative 0; Mismatches 14; Indels 9; Gaps 6;

OY	156	CTGATAGGTATTCGAAACCTTCCCTGCGAACTTCAGAGAACTTCAGCTGATGCGAG	215
	111		111
Db	40	CTGGACAGTATCGAACAACCTTCCCTGCGAACTTCAGAGAACTTCAGCTGATGCGAG	99
OY	216	CTGGACACGAGAGACCGGAAGATTAAGAAACGAGAGATTGACATTCCTGGCTGCACAGTACATC	275
	100	CTGGACACGAGAGACCGGAAGATTAAGAAACGAGAGATTGACATTCCTGGCTGCACAGTACATC	159
OY	276	TTCCACGGTGAAGACGCTGTCTCCACAGCACGCGCTGAGGCGCCTCGAGAACTTCAGAAC	335
Db	160	TTCCACGGTGAAGACGCTGTCTCCACAGCACGCGCGTGAAGCGCTCGAGAAATTCAGAAC	219
OY	336	GCTTACACGAAGTGCAGAAGATACAGTACAGACACAAAGTGCAGCTGGCCATGCAGACTTAC	395
	220	GCTTACACGAAGTGCAGAAGATACAGTACAGACACAAAGTGCAGCTGGCCATGCAGACTTAC	279
OY	396	GAGATGGTGGATTAACACACTTCGAAGGCGTGTATGACAGCTGGCGCGCTTGAACAGAT	455
Db	280	GAGATGGTGGATTAACACACTTTCGAAGGCGTGTATGACAGCTGGCGCGCTTGAACAGAT	339
OY	456	CTGAAGGACAAAGATGGAGGGCAGTATTGTTGAAAGCTCCGAGGGCGAGGGTTAAAAAAA	515
Db	340	CTGAAGGACAAAGATGGAGGGCAGTATTGTTGAAAGCTCCGAGGGCGAGGGTTAAAAAAA	399
OY	516	GCGCGGGGCTCAGAAAGAAAAAGAGGGTCCCGGGGCGCAGAGCAGGACATCAGAGAA	575
Db	400	GCGCGGGGCTCAGAAAGAAAAAGAGGGTCCCGGGGCGCAGAGCAGGACATCAGAGAA	459
OY	576	GACACACCAAGAAAAAGAGCAGCAAGAGGAGGTTGAGTTCTAGTACACCACTTCCTGTTC	635
Db	460	GACACACCAAGAAAAAGAGCAGCAAGAGGAGGTTGAGTTCTAGTACACCACTTCCTGTTC	519
OY	636	GTCGACCCCTCTGATGTGCTGGACATGCCCTGGACCCCAACGAACCCACGTACTGCTCG	695
Db	520	GTCGACCCCTCTGATGTGCTGGACATGCCCTGGACCCCAACGAACCCACGTACTGCTCG	579
OY	696	TGCCACCAAGGTTCTCTATAGGGAGATGATGGCTGTGACATCCAGACGTCCCAATTGAG	755
Db	580	TGCCACCAAGGTTCTCTATAGGGAGATGATGGCTGTGACATCCAGACGTCCCAATTGAG	639
OY	756	TGGTTTCACCTTGGCTGCGTGGACCTTACACGAACCC-AAAGAAAAATGGTTCTGTCC	814
Db	640	TGGTTTCACCTTGGCTGCGTGGACCTTACACGAACCCAAAAAGAAAAATGGTTCTGTTC	699
OY	815	ACGGTGTGCCCGGAAAAAG-AAGAAAGAACTAGAGAGAGCTGTGTG--CCGGATTCGGA	872
Db	700	ACGGTGTGCCCGGAAAAAGAGGAAAGAAAAATAGAGAGAGCTGTGTG--CCGGATTCGGA	759
OY	873	GGAGAA--GTTAATCTGT--CCCTTCATTTCGTCGCA----TATTTCCTCTCTTTAA	926
Db	760	GGAGAAAGGTTAATCTGTGTCCTTCATTCGTGCGAAATATTTCCTCCCTCTCTTTAA	819
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Db	820	AACTAACCTTT 830	

RESULT 8					
LOCUS	BO683118				
DEFINITION	BO683118	905 bp	mRNA	linear	EST 15-JUL-2002
ACCESSION	AGNCNCOURT_8208770	NIH_MGC_112	Homo sapiens	cdna clone	IMAGE:626037B
VERSION	BO683118				
KEYWORDS	BO683118.1	GI:21795797			
SOURCE	EST.				
ORGANISM	human.				
REFERENCE	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	(bases 1 to 905)				


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Db 145 TCCACGGTGAAGACGCTGTCTCCAGACACGCGGTGGAGCCCTGCAGAAATCCAGAAC 208
OY 336 GCCTACAGCAAGTGAAGAAATACAGTACAGACAAAGTGCAGCTGGCTGACAGACTAC 395
Db 209 GCGTACAGCAAGTGAAGAAATACAGTACAGACAAAGTGCAGCTGGCTGACAGACTAC 268
OY 396 GAGATGGTGAATAAACATCTTGAAGGCTTGCAGACCTGGCGGCTTTGAAGCAGAT 455
Db 269 GAGATGGTGAATAAACATCTTGAAGGCTTGCAGACCTGGCGGCTTTGAAGCAGAT 328
OY 456 CTGAGGACAAAGATGAGGAGGAGTGTGAAAGCTCCGAGAGGCGAGAGGCTTAAAAAA 515
Db 329 CTGAGGACAAAGATGAGGAGGAGTGTGAAAGCTCCGAGAGGCGAGAGGCTTAAAAAA 388
OY 516 GCGCGGGGTGAGAAAGAAAAAGAGGCTCCGAGGCGGAGAGCAGAGATCAGAGAA 575
Db 389 GCGCGGGGTGAGAAAGAAAAAGAGGCTCCGAGGCGGAGAGCAGAGATCAGAGAA 448
OY 576 GACACACCAAGAAAAAGAAAGACAAAGAGGCTCTGAGTTCACTGACACCATCTGTCC 635
Db 449 GACACACCAAGAAAAAGAAAGACAAAGAGGCTCTGAGTTCACTGACACCATCTGTCC 508
OY 636 GTGCACCCCTCTGATGCTGACATGCGGTGAGACCCCAAGACCCAGCTACTGCTG 695
Db 509 GTGCACCCCTCTGATGCTGACATGCGGTGAGACCCCAAGACCCAGCTACTGCTG 568
OY 696 TGCACACAGGTCTCTATGAGG-GAGATGATTGCTGATGACATTCACATCTCCAAATGA 754
Db 569 TGCACACAGGTCTCTATGAGGCGAGATGATTGCTGATGACATTCACATCTCCAAATGA 628
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RESULT 10
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DEFINITION AGENCOURT_8208766 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:566982
5', mRNA sequence.
ACCESSION B0678481
VERSION B0678481.1 GI:21791160
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 952)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM2419 row: C column: 03
High quality sequence stop: 592.
Location/Qualifiers
1..952
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/lab_host="DH10B (phage-resistant)"
/Note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(C) Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
SuperScript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 234 a 297 c 257 g 163 t 1 others
ORIGIN

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Query Match 68.2%; Score 653.6; DB 14; Length 952;
Best Local Similarity 95.8%; Pred. No. 1.5e-155;
Matches 682; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

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Db 46 CTGGACAGATCGAAGAACTTCCCTGCACTTCAGAGAACTTCCAGCTGATGCCAGAG 105
OY 216 CTGACACAGAGACGGAAGATGAAGAAAGAGATTGACATCTGCTGACAGATACATC 275
Db 106 CTGGACAGAGAGACGGAAGATGAAGAAAGAGATTGACATCTGCTGACAGATACATC 165
OY 276 TCCACGGTGAAGACGCTGTCTCCAGACACAGCGGTGAGCGCTGCAAGATCCAGAAC 335
Db 166 TCCACGGTGAAGACGCTGTCTCCAGACACAGCGGTGAGCGCTGCAAGATCCAGAAC 225
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OY 396 GAGATGGTGAATAAACATCTTCAAGGCTTGATGACAGACTGGCGGCTTTGAAGCAGAT 455
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Db 346 CTGAAGAGCAAGATGAGAGGAGTATTTGAAAGCTCCGAGAGCGGAGGTTAAAAAA 405
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Db 406 GCGCGGGGTGAGAAAGAAAAAGAGGTCGCCGGCGGAGAGAGATCAGAGAA 465
OY 576 GACACACCAAGAAAAAGAAAGAGAGGCTGAGTTCACTGACACCATCTGTCC 635
Db 466 GACACACCAAGAAAAAGAAAGAGAGGCTGAGTTCACTGACACCATCTGTCC 525
OY 636 GTGCACCCCTCTGATGCTGACATGCGGTGACCCCAAGACCCACGCTACTGCTG 695
Db 526 GTGCACCCCTCTGATGCTGACATGCGGTGACCCCAAGACCCACGCTACTGCTG 585
OY 696 TGCACACAGGTCTCTATGAGGAGATGATTGCTGAGACAATCCACATCTCCAAATGA 755
Db 586 TGCACACAGGTCTCTATGAGGAGATGATTGCTGAGACAATCCACATCTCCAAATGA 645
OY 756 TGGTTTCACTTTGCTGCTGCTGACCTTACCAAGAAAGAAAGAAATGTTCTGTCCA 815
Db 646 TGGTTTCACTTTGCTGCTGCTGACCTTACCAAGAAAGAAAGAAATGTTCTGTCCA 705
OY 816 CGGTGTGTCCAGAG-AAAAGAGAAAGAAAGTGAAGAGAGCTGTGCTGCCG 866
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RESULT 11
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DEFINITION 602707806F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:187664-5
AGCESSION BG749339
VERSION BG749339.1 GI:14059992
KEYWORDS EST.

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Source	Organism	Human
REFERENCE	Homo sapiens	human.
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
JOURNAL	1 (bases 1 to 720)	
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .	
	National Institutes of Health, Mammalian Gene Collection (MGC)	
	unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	
	Email: cgabbs-remail.nih.gov	
	Tissue Procurement: ATCC	
	CDNA Library Preparation: Ling Hong/Rubin Laboratory	
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be	
	found through the I.M.A.G.E. Consortium/LNL at:	
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	EcoRI; CDNA made by Oligo-dT priming. Directionally	
	cloned into EcoRI/XhoI sites using the following 5'	
	adaptor: GGCACGAG(G). Library constructed by Ling Hong	
	in the laboratory of Gerald M. Rubin (University of	
	California, Berkeley) using ZAP-CDNA synthesis kit	
	(Stratagene) and Superscript II RT (Life Technologies).	
	Note: this is a NIH-MGC Library. "	
BASE COUNT	209 a 177 c 212 g 122 t	
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0Y	216 CTGGACACAGAGACGCGAAGATTAAGAAAGCAGACGATTGACATCTCTGCTGACAGATACATC	275
Db	89 CTGGACACAGAGACGCGAAGATTAAGAAAGCAGACGATTGACATCTCTGCTGACAGATACATC	148
0Y	276 TCCACGGTGAAGACCTGTCTCCACACACAGCGCGTGAAGCGCTGACAGAAATGCCAGAAC	335
Db	149 TCCACGGTGAAGACCTGTCTCCACACACAGCGCGTGAAGCGCTGACAGAAATGCCAGAAC	208
0Y	336 GCGTACAGCAAGTGCAGGAATATACAGTACGACAAAGTGCAGCTGGCCATCGACAGACTAC	395
Db	209 GCGTACAGCAAGTGCAGGAATATACAGTACGACCAAAAGTGCAGCTGGCCATCGACAGACTAC	268
0Y	396 GAGATGTGTGATTAACACATTCGAAAGCGTTGATGACAGACTGGCGCGCTTTAAGACAGAT	455
Db	269 GAGATGTGTGATTAACACATTCGAAAGCGTTGATGACAGACTGGCGCGCTTTAAGACAGAT	328
0Y	456 CTGAAGGACAGATGAGAGGCGCGATTTTGAACACTCCGCGAGGCGGAGGGTTAAAAAAA	515
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0Y	516 GGGCGGGGTACAG - AAAGAAAAAAGAGGGTCCCGGGCGCGAGACGAGAGATACAGAG	573
Db	389 GGGCGGGGTACAGACACGAAAAAAGAGGGTCCCGGGCGCGAGACGAGAGATACAGAG	448
0Y	574 AAGACACACAAAGAAAAAGAACCAAAAGAGGCTGTGATGTTCACTGACACCATCTCT	633
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QY	634	CCGTGACACCCCTCTATGTGTGTCGACATGCCCGTGTGACCCCAAGAGAACCCACGTAATGCC	693
Db	509	CCGTGACACCCCTCTATGTGTGTCGACATGCCCGTGTGACCCCAAGAGAACCCACGTAATGCC	568
QY	694	TGTGTCACACAGGTCTGCTATGGAGAGATGATTGGGTGTGACAAATCCACAGTGTCAATTG	753
Db	569	TGTGTCACACAGGTCTGCTATGGAGAGATGATTGGGTGTGACAAATCCACAGTGTCAATTG	628
QY	754	AGTGTGTTTCACCTTTGCTGCGTGCAGACCTTACCCAGAAACCCAAAGGA-AAATGTTCTGT	812
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DEFINITION	B0675901	951 bp	mRNA linear EST 15-JUN-2002
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SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	1 (bases 1 to 951)		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: csapbs-remail.nih.gov		
	Tissue Procurement: DCFD/DFP		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
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	into EcoRI/XhoI sites using the following 5' adaptor:		
	GGCAGCAG(c). Library constructed by Ling Hong in the		
	Laboratory of Gerald M. Rubin (University of California,		
	Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and		
	Superscript II RT (Life Technologies). Note: this is a		
	NIH_MGC Library."		
BASE COUNT	249 a 243 c 304 g 155 t		
ORIGIN			
Query Match	66.4%; Score 635.8; DB 14; Length 951;		
Best Local Similarity	93.6%; Pred. No. 5.1e-151;		
Matches 697; Conservative	0; Mismatches 42; Indels 6; Gaps 3;		
QY	156	CTGATAGTATGATGCAACACTTCCCTGCGAATCTTCAGAGACTTCCACTGATGCGAGAG	215
Db	46	CTGATAGTATGATGCAACACTTCCCTGCGAATCTTCAGAGACTTCCACTGATGCGAGAG	105
QY	216	CTGGACCGAGAGACGGAAGATTAAGAAACGAGATTGACATCTGGCTGCGAGAGTACATC	275


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Db 106 CTGGACAGAGAGAGAGAGAGAGAGAGAGAGATGACATCTGCTGAGAGATCATC 165
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Qy 336 GCGTACAGCAAGTGAAGAGATACATGACAGCAAAAGTGCAGTGCATGCAGACCTAC 395
Db 226 GCGTACAGCAAGTGAAGAGATACATGACAGCAAAAGTGCAGTGCATGCAGACCTAC 285
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Db 646 TGGTTTCCCTTTTCCCTGCGGAGGACCTTACCAGCAAAAGGAAAGTGTCTGTGCC 705
Qy 813 CCAGGAGTGTCCAGAGAAAGAGAGAAAG- TAGGAGAGCTGTGTG - CCGGATC 869
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Db 766 CGAGAGAGCAAGTAAATCTGTCCCTT 790

RESULT 13
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DEFINITION 5' mRNA sequence.
ACCESSION BO677883
VERSION BO677883.1 GI:21790562
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 913)
AUTHORS NIH-MGC Initiative//mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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High quality sequence stop: 607.
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/note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using zap-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 238 a 251 c 293 g 131 t
ORIGIN
Query Match 64.0%; Score 613.2; DB 14; Length 913;
Best Local Similarity 93.9%; Pred. No. 2.8e-145;
Matches 661; Conservative 0; Mismatches 38; Indels 5; Gaps 2;
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Db 46 CTGAGACAGTATCGAAGAACCTTCCCTGCACTTCAGAGAACTTCAGATGCGAGAG 105
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Qy 456 CTGAAGAGCAAGTGAAGAGGAGCAGTATTTGAAGAGCTCCGAGAGGCGAGGTTAAAAAA 515
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Db 406 GCGCGGGGTGAGAAAGAAAGAGGTCGCCGGGCGGAGAGAGAGATCAGAGAA 465
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Qy 811 GTCCACCGTGTCTCCAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
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[illegible]

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D	466	GACACACCAAGAAAAGAAAGACACAAGAGAGGGTGTGAGTTTCACTGACACCATCTGTC	525
OY	636	GTGCAACCCCTTGATGTGCTGGACATGCCCCTGTGACCAACCAAGAACCCACGTACTGCTG	695
D	526	GTGCACCCCTTGATGTGCTGGACATGCCCCTGTGACCAACCAAGAACCCACGTACTGCTG	585
OY	696	TGCCACCAAGGTCTCTAT-GGGGAGATGANT-T-GGTGTGACAATCCACATGCTCCATTG	753
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RESULT	15		
LOCUS	AK007536	1871 bp	mRNA linear HTC 19-JAN-2002
DEFINITION	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:181001Bm11:homolog to CANDIDATE TUDOR SUPPRESSOR P33 INGI HOMOLOG, full insert sequence.		
ACCESSION	AK007536		
VERSION	AK007536.1	GI:12841144	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) 10 day old male pancreas cDNA to mRNA, clone:lib:RIKEN full-length enriched mouse cDNA library clone:181001Bm11.		
ORGANISM	Mus musculus		
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionanthi; Muridae; Musine; Mus.		
REFERENCE	1	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)	
JOURNAL MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	
JOURNAL MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuina,T., Tashiro,H., Itoh,M., Suni,M., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwaqi,K., Fujiwaka,Y., Inoue,K., Togawa,Y., Itawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,D., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)	
JOURNAL MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4	Kawai,J., Shingawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Araiwa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamataka,I.,	

QY 935 TGTTCGTTGATTAAGTA 954
|||
DB 840 ATTTGACTGATATTAAATA 859

Search completed: February 22, 2003, 20:52:03
Job time : 2261 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 19:25:28 : Search time 4159 Seconds
(Without alignments)
5791.417 Million cell updates/sec

Title: US-09-442-013-7

Perfect score: 958
Sequence: 1 ttgtcgtacctcagccctgc.....cgtttactactagtaacaa 958

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Result				SUMMARIES		Description
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3	798.4	83.3	1108	18	US-09-442-013-1	Sequence 1, Appl
4	794.6	82.9	1073	28	US-09-716-972-4875	Sequence 4875, Ap
5	794.6	82.9	1073	29	US-09-721-588-5351	Sequence 5351, Ap
6	794.6	82.9	967	69	US-60-250-830-3236	Sequence 3236, Ap
7	794.6	82.9	2537	76	US-60-323-966-3236	Sequence 3236, Ap
8	787.4	82.2	807	18	US-09-442-013-3	Sequence 3, Appl
9	787.4	82.2	807	18	US-09-442-013-5	Sequence 5, Appl
10	771	80.5	1082	1	PCT-US02-25465-43	Sequence 43, Appl
11	647.4	67.6	958	18	US-09-442-013-9	Sequence 9, Appl
12	645.6	67.4	1275	62	US-60-184-797-652	Sequence 652, App
13	645.6	67.4	1275	71	US-60-278-258-16936	Sequence 16936, A
14	641.8	67.0	1465	1	PCT-US01-04098A-646	Sequence 646, App
15	641.8	67.0	1465	24	US-09-620-325-298	Sequence 298, App
16	622	64.9	1011	20	US-09-532-645-18	Sequence 18, Appl
17	622	64.9	1011	56	US-60-126-246-5	Sequence 5, Appl
18	449.4	46.9	1199	1	PCT-US01-03600A-924	Sequence 924, App
19	449.4	46.9	1199	1	PCT-US01-04098A-2614	Sequence 2614, Ap
20	449.4	46.9	1199	18	US-09-496-914A-7985	Sequence 7985, Ap
21	449.4	46.9	1199	22	US-09-560-875A-7985	Sequence 7985, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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33 376.6 39.3 456 34 US-09-904-809-9815 Sequence 9815, Ap
34 376.6 39.3 456 34 US-09-918-995-16047 Sequence 16047, A
35 376.6 39.3 456 34 US-09-925-564-32620 Sequence 32620, A
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37 361.2 37.7 443 18 US-10-235-926-2828 Sequence 13363, A
38 351.6 36.7 428 36 US-09-975-673A-13363 Sequence 13363, A
39 351.6 36.7 428 36 US-09-975-673A-13363 Sequence 13363, A
40 351.6 36.7 435 18 US-09-496-911-13364 Sequence 13364, A
41 351.6 36.7 435 18 US-09-975-673A-13364 Sequence 13364, A
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44 346 36.1 402 34 US-09-904-013-4047 Sequence 2963, Ap
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ALIGNMENTS

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RESULT 1
US-09-442-013-7
; Sequence 7, Application US/09442013
; GENERAL INFORMATION:
; APPLICANT: Lou, Ying
; APPLICANT: Xu, Xiang
; APPLICANT: Leo, Cindy
; APPLICANT: Huang, Betty
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: A-68289/DJ/RMS/DAY
; CURRENT APPLICATION NUMBER: US/09/442, 013
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-442-013-7
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Query Match 100.0%; Score 958; DB 18; Length 958;
Best Local Similarity 100.0%; Pred. No. 3,3e-247;
Matches 958; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 TGGAGCAAGAGTCACTCCACGAGACTTGAGAGCTGATGATGAGAACTTCCCT 180
DB 121 TGGAGCAAGAGTCACTCCACGAGACTTGAGAGCTGATGATGAGAACTTCCCT 180
QY 181 GCGAAGTTCAGAGAACTTCCAGCTGATGAGAGCTGAGCAAGAGAGGAGGAGATAGA 240
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QY 241 AAGCAGAGATTGATCTGCTGCTGAGAGTACATCTCCAGGCTGAAGACCGCTGTCCAG 300
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RESULT 2
US-09-799-451-403
; Sequence 403, Application US/09799451
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qiang A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yuning
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
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: CURRENT FILING DATE: 2001-03-05
: NUMBER OF SEQ ID NOS: 948
: SOFTWARE: PL_FL_genes Version 2.0
: SEQ ID NO 403
: LENGTH: 1300
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (188)..(913)
US-09-799-451-403

Query Match 97.7%; Score 936.4; DB 30; Length 1300;
Best Local Similarity 98.8%; Pred. No. 2,5e-241;
Matches 943; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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RESULT 3
US-09-442-013-1
; Sequence 1, Application US/09442013
; GENERAL INFORMATION:
; APPLICANT: Lou, Yang
; APPLICANT: Xu, Xiang
; APPLICANT: Leo, Cindy
; APPLICANT: Huang, Betty
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
; FILE REFERENCE: A-68289/DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/442.013
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1108
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-442-013-1

Query Match 83.3%; Score 798.4; DB 18; Length 1108;
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DB 721 AGAGAGAGACACCAAGAAAAAGAGACAAAGAGAGGCTGTGAGTTCACTGACACCAT 780
OY 629 CCTGTCCGTCACCCCTCTGATGTGCTGGAACATGCGCGGAGACCAAGAGAAACCAAGTA 688
DB 781 CCTGTCCGTCACCCCTCTGATGTGCTGGAACATGCGCGGAGACCAAGAGAAACCAAGTA 840
OY 689 CTGACCTGTGCCACACAGGCTCTCTATGAGGAGATGATGAGTGTGACAAATCCAGACTGTCC 748
DB 841 CTGACCTGTGCCACACAGGCTCTCTATGAGGAGATGATGAGTGTGACAAATCCAGACTGTCC 900

QY	749	AATTGACGTGGTTTCACCTTTTCCCTGCGTGACCTTACACGAATCCCAAGAAATGGTT	808
Db	901	AATTGAGTGGTTTCACCTTTTCCCTGCGTGACCTTACACGAATCCCAAGAAATGGTT	960
QY	809	CTGTGCACGGTGTGTGCCAGGAAAAAGAGAAAGAAGTATGAGAGAGCTGTGTGCCCGAT	868
Db	961	CTGTGCACGGTGTGTGCCAGGAAAAAGAGAAAGAAGTATGAGAGAGCTGTGTGCCCGAT	1020
QY	869	CCGAGGAGCAAGTTAATCTGTCCCTTCATTTCGTGTGCAATATTTTCCTCTTTTAAAA	928
Db	1021	CCGAGGAGCAAGTTAATCTGTCCCTTCATTTCGTGTGCAATATTTTCCTCTTTTAAAA	1080
QY	929	CTACCTGTTCGGTTGTACTTAGTATAC	956
Db	1081	CTACCTGTTCGGTTGTACTTAGTATAC	1108

```

RESULT 4
US-09-716-972-4875
: Sequence 4875, Application US/09716972
: GENERAL INFORMATION:
: APPLICANT: Hunter, John J.
: APPLICANT: Shyjan, Andrew W.
: APPLICANT: Vasicsek, Thomas
: APPLICANT: lee, John
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600, 2030-001
: CURRENT APPLICATION NUMBER: US/09/716,972
: CURRENT FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 60/166,948
: PRIOR FILING DATE: 1999-11-22
: NUMBER OF SEQ ID NOS: 5251
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4875
: LENGTH: 1073
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-716-972-4875

```

Query Match	82.9%;	Score 794.6;	DB 28;	Length 1073;
Best Local Similarity	99.5%;	Pred. No. 4e-203;		
Matches 797; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	156	CTGATAGGTATTCGAAACCTTCCCTGGCAATTCACAGAAATTCCAGCTGATGCAGAG	215
Db	38	CTGGACAGTATTCGAAGAACCTTCCCTGGCAATTCACAGAAACTTCCAGCTGATGCCAGAG	97
QY	216	CTTGACACGAGAGCGAAGATTAAGAAGCAGAGATTGACATCTCTGGCTGCAGAGTACATC	275
Db	98	CTGGACACGAGAGCGAAGATTAAGAAGCAGAGATTGACATCTCTGGCTGCAGAGTACATC	157
QY	276	TTCACGGTGAAGACGCTGTCTCCAGACCAGCGCTGGAGCGCTGCAGAAAGATCCAGAAC	335
Db	158	TTCACGGTGAAGACGCTGTCTCCAGACCAGCGCTGGAGCGCTGCAGAAAGATCCAGAAC	217
QY	336	GCCATACAGCATGTCACAAGGAATACAGTAGAGACACAAAATGTCAGTGGGCATCATGACACTTAC	395
Db	218	GCCATACAGCATGTCACAAGGAATACAGTAGAGACACAAAATGTCAGTGGGCATCATGACACTTAC	277
QY	396	GAGATGCTGATTAACACATTTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT	455
Db	278	GAGATGCTGATTAACACATTTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT	337
QY	456	CTGAAGCAACAGATGAGAGGCGACGTGATTTTGAAGCTCCGAGAGGCGAGGGCTTAAAAAAA	515
Db	338	CTGAAGCAACAGATGAGAGGCGACGTGATTTTGAAGGCTCCGAGAGGCGAGGGCTTAAAAAAA	397
QY	516	GGCCGGGGTTCAGAAAGAAAAAGAGGGTCCCGGGGCGCGAGAGCGAGAGATCAGAGGAA	575
Db	398	GGCCGGGGTTCAGAAAGAAAAAGAGGGTCCCGGGGCGCGAGAGCGAGAGATCAGAGGAA	457

OY	576	GAAACACCAAGAAAAAAGAACACAAAAAGAGAGGTCGTGATTTCACTGACACATCTGTCC	635
Db	458	GACACACCAAGAAAAAAGAACACAAAAAGAGAGGTCGTGATTTCACTGACACATCTGTCC	517
OY	636	GTGCACCCCTCTGATGTGCTGGACATGCCGTGGACCCAAACGAACCCACGTACTGCTTG	695
Db	518	GTGCACCCCTCTGATGTGCTGGACATGCCGTGGACCCAAACGAACCCACGTACTGCTTG	577
OY	656	TGCCACCAAGGTCCTCTATGGGGAATGATTGGCTGTACAATCCAGACTGTCCAATTTGAG	755
Db	578	TGCCACCAAGGTCCTCTATGGGGAATGATTGGCTGTACAATCCAGACTGTCCAATTTGAG	637
OY	756	TGGTTTCACTTTGCTGCTGGAGACTTACCAAGAACCCAAAGGAAATGGTCTGTCCA	815
Db	638	TGGTTTCACTTTGCTGCTGGAGACTTACCAAGAACCCAAAGGAAATGGTCTGTCCA	697
OY	816	CGGTCTGTCCAGAAAGAGAAAGAGAGAGAGCTGTGTGCCCGGATCCGAGGA	875
Db	698	CGGTCTGTCCAGAAAGAGAAAGAGAGAGAGCTGTGTGCCCGGATCCGAGGA	757
OY	876	GCAAGTTATCTGTGCCCTTCAATTGTGTGCCAATATTTCCTTCCTTTTAAACTTACTT	935
Db	758	GCAAGTTATCTGTGCCCTTCAATTGTGTGCCAATATTTCCTTCCTTTTAAACTTACTT	817
OY	936	GTTCGCTGATCTTACTGTAAC	956
Db	818	GTTCGCTGATCTTACTGTAAC	838

```

RESULT 5
US-09-721-588-5351
: SEQUENCE 5351, Application US/09721588
: GENERAL INFORMATION:
: APPLICANT: Gearling, David P.
: APPLICANT: Holtzman, Douglas A.
: APPLICANT: Villaveja, Jean-Luc
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MO
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600.2046-001
: CURRENT APPLICATION NUMBER: US/09/721,588
: CURRENT FILING DATE: 2000-11-22
: PRIOR APPLICATION NUMBER: 60/167,381
: PRIOR FILING DATE: 1999-11-24
: NUMBER OF SEQ ID NOS: 5410
: SOFTWARE: FASTSEQ for Windows Version 4.0.
: SEQ ID NO 5351
: LENGTH: 1073
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-721-588-5351

```

Query Match	82.98;	Score 794.6;	DB 29;	Length 1073;
Best Local Similarity	99.58;	Pred. No. 4e-203;		
Matches 797;	Conservative	0;	Mismatches 4;	Indels 0;
			Gaps	0;

Oy	156	CTGATAGTATTCGAAACCTTCCCTCGGAATTCAGAGAAATCTCCAGCTGATGCGGAG	215
Db	38	CTGGACAGTATTCGAAACCTTCCCTGGAACTTCAGAGAAATCTCCAGCTGATGCGGAG	97
Oy	216	CTGGACCGAGACAGGAAGATATAAAGCAGAGATTACATTCTCGCTGAGAGTATATC	275
Db	98	CTGGACCGAGAGCGGAAGATATAAAGCAGAGATTACATTCTCGCTGAGAGTATATC	157
Oy	276	TCCACGCGTGAAGACGCTGTCTCCAGACCAGCGCGCTGGAGCGCTGCAGAGATCCAGAAC	335
Db	158	TCCACGCGTGAAGACGCTGTCTCCAGACCAGCGCGCTGGAGCGCTGCAGAGATCCAGAAC	217
Oy	336	GCCATACACCAAGTCCCAAGGAATTACAGTGCAGCAAAATGTGACGTGGCCATGACGACCTAC	395
Db	218	GCCATACCAAGTCCCAAGGAATTACAGTGCAGCAAAATGTGACGTGGCCATGACGACCTAC	277
Oy	396	GAGATGCTGATTAACACATTCGAAAGCGTTGATGCAGACCTGGCGCGCTTGAAGCAGAT	455

Dh 278 GAGATGTTGATTAACACATTTCGAAGGCTTATGACAGCTTGGCCGCTTTGAAGCAGAT 337
Qy 456 CTGAAGACCAATGAGAGGCGATGATTTTGAAGCTCCGGAGGGCGAGGGTTAAAGAA 515
Dh 338 CTGAAGACCAATGAGAGGCGATGATTTTGAAGCTCCGGAGGGCGAGGGTTAAAGAA 397
Qy 516 GGGCGGGGTCAGAAAAAGAGGGTCCCGGGGCCGAGGCGAGAGGACATCAGAGGAA 575
Dh 398 GGGCGGGGTCAGAAAAAGAGGGTCCCGGGGCCGAGGCGAGAGGACATCAGAGGAA 457
Qy 576 GACACACCAAGAAAAAGAGACACAAGAGGGTCTGATTCCTGACACCATCTCTGC 635
Dh 458 GACACACCAAGAAAAAGAGACACAAGAGGGTCTGATTCCTGACACCATCTCTGC 517
Qy 636 GTGACACCCCTGATGTTGTCGACATGCCCGTGACCCCAAGCAACCCACGACTGCTG 695
Dh 518 GTGACACCCCTGATGTTGTCGACATGCCCGTGACCCCAAGCAACCCACGACTGCTG 577
Qy 696 TGCCACACAGTCTCTATGGGAGATGATGTCGTCGACAAATCCAGACTGTCCAAATTGAG 755
Dh 578 TGCCACACAGTCTCTATGGGAGATGATGTCGTCGACAAATCCAGACTGTCCAAATTGAG 637
Qy 756 TGGTTTCACTTTGCTGCTGGTGACCTTACACAGAAACCCAAAGAAAATGTTCTGTCCA 815
Dh 638 TGGTTTCACTTTGCTGCTGGTGACCTTACACAGAAACCCAAAGAAAATGTTCTGTCCA 697
Qy 816 CGGTGTCTCCAGAAAAAGAGAAAGTAGAGAGAGCTGTGTGCCCGGATCCGAGAGA 875
Dh 698 CGGTGTCTCCAGAAAAAGAGAAAGTAGAGAGAGCTGTGTGCCCGGATCCGAGAGA 757
Qy 876 GCAAGTTAATCTGTCCTTCATTCGTCGCAATATTCCCTCTTTAAACTACTCTT 935
Dh 758 GCAAGTTAATCTGTCCTTCATTCGTCGCAATATTCCCTCTTTAAACTACTCTT 817
Qy 936 GTTCGGTTGATTAAGTAAC 956
Dh 818 GTTCGGTTGATTAAGTAAC 838

RESULT 6
; Sequence 3236, Application US/60250830
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0020 P
; CURRENT APPLICATION NUMBER: US/60/250,830
; CURRENT FILING DATE: 2000-11-04
; NUMBER OF SEQ ID NOS: 3246
; SOFTWARE: PERL Program
; SEQ ID NO 3236
; LENGTH: 2537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 121128.18
US-60-250-830-3236

Query Match 82.9%; Score 794.6; DB 69; Length 2537;
Best Local Similarity 99.5%; Pred. No. 5.3e-203;
Matches 797; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 156 CTGATAGTATCGAGAACTTCCTGCGAATTCGAGAGAACTTCACCTATGCGAGAG 215
Dh 56 CTGACACTATCGAGAACTTCCTGCGAATTCGAGAGAACTTCACCTATGCGAGAG 115
Qy 216 CTGACACGAGAGAGAGATAGAAAGCAGAGATTGACATCTGCTGCGAGAGATATC 275
|||||

Dh 116 CTGACACGAGAGACGGAAGATAGAAACAGAGATTGACATCTGTGCTGACAGATATATC 175
Qy 276 TCCACGGTGAAGAGCGCTGCTCCAGACAGCGCGTGGAGCGCTGCGACAGATCCAGAAC 335
Dh 176 TCCACGGTGAAGAGCGCTGCTCCAGACAGCGCGTGGAGCGCTGCGACAGATCCAGAAC 235
Qy 336 GCGTACACCAAGTGCAGAAATATACAGTACACAAAGTACAGTACAGTACAGTACAGTAC 395
Dh 236 GCGTACACCAAGTGCAGAAATATACAGTACACAAAGTACAGTACAGTACAGTACAGTAC 295
Qy 396 GAGATGTTGATTAACACATTTCGAAGGCTTATGACAGCTTGGCGGCTTTGAAGCAGAT 455
Dh 296 GAGATGTTGATTAACACATTTCGAAGGCTTATGACAGCTTGGCGGCTTTGAAGCAGAT 355
Qy 456 CTGAAGACCAATGAGAGGCGATGATTTTGAAGCTCCGGAGGGCGAGGGTTAAAGAA 515
Dh 356 CTGAAGACCAATGAGAGGCGATGATTTTGAAGCTCCGGAGGGCGAGGGTTAAAGAA 415
Qy 516 GGGCGGGGTCAGAAAAAGAGGGTCCCGGGGCCGAGGCGAGAGGACATCAGAGGAA 575
Dh 416 GGGCGGGGTCAGAAAAAGAGGGTCCCGGGGCCGAGGCGAGAGGACATCAGAGGAA 475
Qy 576 GACACACCAAGAAAAAGAGACACAAGAGAGGTCGATTCCTGACACCATCTCTGC 635
Dh 476 GACACACCAAGAAAAAGAGACACAAGAGAGGTCGATTCCTGACACCATCTCTGC 535
Qy 636 GTGACACCCCTGATGTTGTCGACATGCCCGTGACCCCAAGCAACCCACGACTGCTG 695
Dh 536 GTGACACCCCTGATGTTGTCGACATGCCCGTGACCCCAAGCAACCCACGACTGCTG 595
Qy 696 TGCCACACAGTCTCTATGGGAGATGATGTCGTCGACAAATCCAGACTGTCCAAATTGAG 755
Dh 596 TGCCACACAGTCTCTATGGGAGATGATGTCGTCGACAAATCCAGACTGTCCAAATTGAG 655
Qy 756 TGGTTTCACTTTGCTGCTGGTGACCTTACACAGAAACCCAAAGAAAATGTTCTGTCCA 815
Dh 656 TGGTTTCACTTTGCTGCTGGTGACCTTACACAGAAACCCAAAGAAAATGTTCTGTCCA 715
Qy 816 CGGTGTCTCCAGAAAAAGAGAAAGTAGAGAGAGCTGTGTGCCCGGATCCGAGAGA 875
Dh 716 CGGTGTCTCCAGAAAAAGAGAAAGTAGAGAGAGCTGTGTGCCCGGATCCGAGAGA 775
Qy 876 GCAAGTTAATCTGTCCTTCATTCGTCGCAATATTCCCTCTTTAAACTACTCTT 935
Dh 776 GCAAGTTAATCTGTCCTTCATTCGTCGCAATATTCCCTCTTTAAACTACTCTT 835
Qy 936 GTTCGGTTGATTAAGTAAC 956
Dh 836 GTTCGGTTGATTAAGTAAC 856

RESULT 7
; Sequence 3236, Application US/60323966
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0020-1 P
; CURRENT APPLICATION NUMBER: US/60/323,966
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 3246
; SOFTWARE: PERL Program
; SEQ ID NO 3236
; LENGTH: 2537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 121128.18

US-60-323-966-3236

Query Match 82.9%; Score 794.6; DB 76; Length 2537;
Best Local Similarity 99.5%; Pred. No. 5.3e-203;
Matches 797; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 156 CTGATAGTATCGAGAACCTTCCTCGCAACTTCAGAGAACTTCAGCTGATGCGAGAG 215
DB 56 CTGGACAGTATCGAGAACCTTCCTCGCAACTTCAGAGAACTTCAGCTGATGCGAGAG 115
QY 216 CTGGACCAAGACGGAATAAGAAAGACAGAGATGACATCTGCTGCTGACAGTACATC 275
DB 116 CTGGACCAAGACGGAATAAGAAAGACAGAGATGACATCTGCTGCTGACAGTACATC 175
QY 276 TCCACGCTGAAGACGCTGCTCCAGACACGCGCTGAGCGCTCGAGAAATCCAGAC 335
DB 176 TCCACGCTGAAGACGCTGCTCCAGACACGCGCTGAGCGCTCGAGAAATCCAGAC 235
QY 336 GCGTACAGCAAGTGCAGAGATACAGTACGACAAAGTCCAGCTGCCATGCACTAC 395
DB 236 GCGTACAGCAAGTGCAGAGATACAGTACGACAAAGTCCAGCTGCCATGCACTAC 295
QY 396 GAGATGCTGATTAACACATCTGGAAGCTTTGATGACAGCTGGCGCTTTGAAGACAT 455
DB 296 GAGATGCTGATTAACACATCTGGAAGCTTTGATGACAGCTGGCGCTTTGAAGACAT 355
QY 456 CTGAAGACAAAGTGGAGGCGAGTATTTGAAAGCTCCGAGAGGCGAGGTTAAAAA 515
DB 356 CTGAAGACAAAGTGGAGGCGAGTATTTGAAAGCTCCGAGAGGCGAGGTTAAAAA 415
QY 516 GCGCGGGGTGAGAAAGAAAAAGGGTCCCGGGGCCGAGGCGAGAGACATCAGAGAA 575
DB 416 GCGCGGGGTGAGAAAGAAAAAGGGTCCCGGGGCCGAGGCGAGAGACATCAGAGAA 475
QY 576 GACACACCAAGAAAGAAAGCAAGAGAGGCTGATGCTTCACTACACATCTCTGTC 635
DB 476 GACACACCAAGAAAGAAAGCAAGAGAGGCTGATGCTTCACTACACATCTCTGTC 535
QY 636 GTGCACCCCTGATGCTGTCGACATGCCGTCGACCCCAAGCAACCCAGTACTGCTG 695
DB 536 GTGCACCCCTGATGCTGTCGACATGCCGTCGACCCCAAGCAACCCAGTACTGCTG 595
QY 696 TGGCACACAGCTCTCTATGAGGAGATGATGGCTGTGACAAATCCAGACTGTCCAATT 755
DB 596 TGGCACACAGCTCTCTATGAGGAGATGATGGCTGTGACAAATCCAGACTGTCCAATT 655
QY 756 TGGTTCACTTGGCCGCGGAGACCTTACACGAAACCCAAAGGAAATGGTCTGTCCA 815
DB 656 TGGTTCACTTGGCCGCGGAGACCTTACACGAAACCCAAAGGAAATGGTCTGTCCA 715
QY 816 CGGTGTCTCAGGAAAGAGAGAGAGTAGAGAGCTGTGTCCCGATCCGAGCA 875
DB 716 CGGTGTCTCAGGAAAGAGAGAGAGTAGAGAGCTGTGTGTCCCGATCCGAGCA 775
QY 876 GCAAGTTAATCTGTCCCTTCATTCGTGTGCAATATTTCCCTTCCTTTAAACCTAC 935
DB 776 GCAAGTTAATCTGTCCCTTCATTCGTGTGCAATATTTCCCTTCCTTTAAACCTAC 835
QY 936 GTTCGGTTGATCTTACTAGTAAC 956
DB 836 GTTCGGTTGATCTTACTAGTAAC 856

RESULT 8

US-09-442-013-3

; Sequence 3, Application US/09442013

; GENERAL INFORMATION:

; APPLICANT: Lou, Yang

; APPLICANT: Xu, Xiang

; APPLICANT: Leo, Cindy

; APPLICANT: Huang, Betty

; APPLICANT: Shen, Mary

; TITLE OF INVENTION: NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS

; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: A-68289/DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/442,013
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-442-013-3

Query Match 82.2%; Score 787.4; DB 18; Length 807;
Best Local Similarity 98.6%; Pred. No. 3.2e-201;
Matches 794; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 TGTGACCTCAGCCCTGCTGCGGCGATTTGAGAGGTCTGCTGCTGAGCATCCAGTCTCC 62
DB 1 TGTGACCTCAGCCCTGCTGCGGCGATTTGAGAGGTCTGCTGCTGAGCATCCAGTCTCC 60
QY 63 TTGCTACTGCACTGACAGCTCAGGCTGATTTCCAGCACTGTCTGTCAGAGCAATG 122
DB 61 TTGCTACTGCACTGACAGCTCAGGCTGATTTCCAGCACTGTCTGTCAGAGCAATG 120
QY 123 GGAGCAAGAGTCACTCCAGAGACTCTGAGAGGCTGATGATGATGAGAACTTCCCTGC 182
DB 121 GGAGCAAGAGTCACTCCAGAGACTCTGAGAGGCTGATGATGATGAGAACTTCCCTGC 180
QY 183 GAACCTCAAGAGAACTTCCAGAGCTGATGCGAGAGCTTGACCAAGAGCGGAACATAAGAA 242
DB 181 GAACCTCAAGAGAACTTCCAGAGCTGATGCGAGAGCTTGACCAAGAGCGGAACATAAGAA 240
QY 243 GCAGAGATTGACATCTGCTGCTGAGAGTACATCTCCAGGCTGAGAGAGCTGTCTCCAGAC 302
DB 241 GCAGAGATTGACATCTGCTGCTGAGAGTACATCTCCAGGCTGAGAGAGCTGTCTCCAGAC 300
QY 303 CAGCGGCTGAGGCGCTGAGAGAGATCCAGAACGCTTACAGCAAGTGCAGAGATACACT 362
DB 301 CAGCGGCTGAGGCGCTGAGAGAGATCCAGAACGCTTACAGCAAGTGCAGAGATACACT 360
QY 363 GACGAAAGTGCAGTGGCCATGCGAGACTGAGAGTGAATGATGATTAACATTCGAAAG 422
DB 361 GACGAAAGTGCAGTGGCCATGCGAGACTGAGAGTGAATGATGATTAACATTCGAAAG 420
QY 423 CTGTGATGACAGCTGCTGCGGCTTTGAAGCAGATCTGAAAGACAAATGAGGCGACTGAT 482
DB 421 CTGTGATGACAGCTGCTGCGGCTTTGAAGCAGATCTGAAAGACAAATGAGGCGACTGAT 480
QY 483 TTTGAAAGCTCGGAGGCGAGGCTTTAAAAAAGCCCGGGGTGAGAAAGAAAAAGAGGG 542
DB 481 TTTGAAAGCTCGGAGGCGAGGCTTTAAAAAAGCCCGGGGTGAGAAAGAAAAAGAGGG 540
QY 543 TCCCGGGGCGAGGCGAGAGGAGATCAGAGGAACACACCAAGAAAAAGAAAGCAAA 602
DB 541 TCCCGGGGCGAGGCGAGAGGAGATCAGAGGAACACACCAAGAAAAAGAAAGCAAA 600
QY 603 GGAGGCTGAGAGTCTCAACACATCTGCTGCTGACACCCCTGATGCTGTCAGCATG 662
DB 601 GGAGGCTGAGAGTCTCAACACATCTGCTGCTGACACCCCTGATGCTGTCAGCATG 660
QY 663 CCCGTGAGCCCAAGAACCAAGTACTGCTGCTGACACAGGCTCTATGAGGAGATG 722
DB 661 CCCGTGAGCCCAAGAACCAAGTACTGCTGCTGACACAGGCTCTATGAGGAGATG 720
QY 723 ATTTGGCTGTGACATCAACAGCTGCTCAATTTGAGTGTTCACCTTTCGCTGAGACTT 782
DB 721 ATTTGGCTGTGACATCAACAGCTGCTCAATTTGAGTGTTCACCTTTCGCTGAGACTT 780
QY 783 ACCAGAAACCCCAAGAAATGCT 807
DB 781 ACCAGAAACCCCAAGAAATGCT 805

```

RESULT 9
US-09-442-013-5
; Sequence 5, Application US/09442013
; GENERAL INFORMATION:
; APPLICANT: Lou, Ying
; APPLICANT: Xu, Xiang
; APPLICANT: Leo, Cindy
; APPLICANT: Huang, Betty
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: NOVEL IAPs ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: A-68289/DJB/RMS/DAY
; CURRENT APPLICATION NUMBER: US/09/442,013
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-442-013-5

```

Query Match	82.2%;	Score 787.4;	DB 18;	Length 807;
Best Local Similarity	98.6%;	Pred. No. 3.2e-201;		
Matches 794; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;

OY	3	TGTCGACCTCAGCCCTCGCGTGGGCGCTATTGAGGGTCTGCGGCTGAGCATTCAGTGTCC	62
Db	1	TGCTACCTCACCCTCTGGCGTGGGCGATAGGAGGCTCTGGCTGGAGCATTCAGTGTCC	60
OY	63	TTCCGACGCGCCCTACAGACGCTCAGGCGCGATTTCACGACCTGTGTCCAGACCAATG	122
Db	61	TTTCGACTGCGCCTACACACGCTCAGGCGCTGATTTCCAGCAGCTGTGTTCAGGACCAATG	120
OY	123	GGAGCAAGAGTCACTCCACGAGACTCTGAGGCGCTGATAGTATGAGAACCTTCCCTGC	182
Db	121	GGAGCAAGAGTCACTCCACAGACACTCTGGAGCGCTGATAGTATGAGAACCTTCCCTGC	180
OY	183	GAACCTCAGAGCACTTCCAGCTGATGTGGAGAGCGTGGAGCCAGAGGACGGAAATTAAGAA	242
Db	181	GAACCTCAGAGCACTTCCAGCTGATGTGGAGAGCTGGAGCCAGAGGACGGAAATTAAGAA	240
OY	243	GCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCAGGTGAAGACGCTGTCTCCAGAC	302
Db	241	GCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCAGGTGAAGACGCTGTCTCCAGAC	300
OY	303	CAGCGCGTGGAGCGGCTGCAGAGATGCCAGAAAGCGCTACAGCAATGCAGGAATATCACT	362
Db	301	CAGCGCGTGGAGCGGCTGCAGAGATGCCAGAAAGCGCTACAGCAAGTGCAGGAATATCACT	360
OY	363	GAACGCAAAAGTGCACCTGGCCATGCAGACCTACGAGATGTGGATTAACACATTTGGAAG	422
Db	361	GAACGCAAAAGTGCACCTGGCCATGCAGACCTACGAGATGTGGATTAACACATTTGGAAG	420
OY	423	CTTGTATGCAGACCTGGCGCGCTTTTAAGCAAGTCTGAAAGGACAAAGATGAGGGCAGTAT	482
Db	421	CTTGTATGCAGACCTGGCGCGCTTTTAAGCAAGTCTGAAAGGACAAAGATGAGGGCAGTAT	480
OY	483	TTTGAAGCTCCGAGGAGCGAGGTTTAAAAAAGCGCGGAGTCAAGAAAGAAAAAGAGG	542
Db	481	TTTGAAGCTCCGAGGAGCGAGGTTTAAAAAAGCGCGGAGTCAAGAAAGAAAAAGAGG	540
OY	543	TCCCGGGGCGCAGGCGAGGAGCATTCAGAGAAACACACCAAGAAAAAAGAGCAAAA	602
Db	541	TCCCGGGGCGCAGGCGAGGAGCATTCAGAGAAAGACACCAAGAAAAAAGAGCAAAA	600
OY	603	GGAGGGTCTGATTTCACTATCACACATCCGTCCGAGACACCCCTGTGATGTGCTGGACATG	662
Db	601	GGAGGGTCTGATTTCACTATCACACATCCGTCCGAGACACCCCTGTGATGTGCTGGACATG	660
OY	663	CCCGTGGACCCAAAGCAACCCAGTACTGCTGTGCCACACAGGCTCTCTATGGGAGATG	722
Db	661	CCCGTGGACCCAAAGCAACCCAGTACTGCTGTGCCACACAGGCTCTCTATGGGAGATG	720

Qy	723	ATTGCTCTGTGACAAATCCAGACTGTCCAAATTAGTGTGTTTCACTTTGGCTCGGTGGACCTT	782
Db	721	ATTGGCTCTGTGCAATCCAGACTGTCCAAATTAGTGTGTTTCACTTTGGCTCGGTGGACCTT	780
Qy	783	ACCACGAAACCCAAAGAAATGCT	807
Db	781	ACCACGAAACCCAAAGAAATGCT	805

```

RESULT 10
: PCT-US02-25465-43
: Sequence 43, Application PC/TUS0225465
: GENERAL INFORMATION:
: APPLICANT: INCYTE GENOMICS, INC.
: APPLICANT: AZIMZAI, Yalda
: APPLICANT: BARROSO, Ines
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: BECHA, Shanya D.
: APPLICANT: BOROWSKY, Mark L.
: APPLICANT: DUGGAN, Brendan M.
: APPLICANT: ELLIOTT, Vicki S.
: APPLICANT: EMERLING, Brooke M.
: APPLICANT: FORSYTHE, Ian J.
: APPLICANT: GIERZEN, Kimberly J.
: APPLICANT: GORVAD, Ann E.
: APPLICANT: GRAUL, Richard C.
: APPLICANT: GRIFFIN, Jennifer A.
: APPLICANT: GURURAJAN, Rajagopal
: APPLICANT: HAFALIA, April J.A.
: APPLICANT: ISON, Craig H.
: APPLICANT: KABLE, Amy E.
: APPLICANT: KHAN, Farrah A.
: APPLICANT: LEE, Sally
: APPLICANT: LEE, Soo Yeun
: APPLICANT: LI, Joana X.
: APPLICANT: REDDY, Roopa
: APPLICANT: RICHARDON, Thomas W.
: APPLICANT: SPRAGUE, William W.
: APPLICANT: SMARNAKAR, Anita
: APPLICANT: TANG, Y. Tom
: APPLICANT: WARREN, Bridget A.
: APPLICANT: XU, Yuming
: APPLICANT: YAO, Monique G.
: APPLICANT: YUE, Henry
: APPLICANT: YUE, Huibin
: TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEA
: FILE REFERENCE: PF-1126 PCT
: CURRENT APPLICATION NUMBER: PCT/US02/25465
: CURRENT FILING DATE: 2002-08-08
: PRIOR APPLICATION NUMBER: US 60/311,017
: PRIOR FILING DATE: 2001-08-08
: PRIOR APPLICATION NUMBER: US 60/313,070
: PRIOR FILING DATE: 2001-08-17
: PRIOR APPLICATION NUMBER: US 60/313,071
: PRIOR FILING DATE: 2001-08-17
: PRIOR APPLICATION NUMBER: US 60/314,678
: PRIOR FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/316,692
: PRIOR FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: US 60/317,913
: PRIOR FILING DATE: 2001-09-07
: PRIOR APPLICATION NUMBER: US 60/322,182
: PRIOR FILING DATE: 2001-09-14
: PRIOR APPLICATION NUMBER: US 60/340,747
: PRIOR FILING DATE: 2001-12-07
: PRIOR APPLICATION NUMBER: US 60/342,761
: PRIOR FILING DATE: 2001-12-20
: PRIOR APPLICATION NUMBER: US 60/369,129
: PRIOR FILING DATE: 2002-03-29
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PERL Program
: SEQ ID NO 43

```

```
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 72332548CB1
PCT-US02-25465-43
```

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Query Match      80.5%; Score 771; DB 1; Length 1082;
Best Local Similarity 99.1%; Pred. No. 9.3e-197;
Matches 796; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
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```
Oy 156 CTGATAGTATCGAGAACCTTCCTCGCAACTTCAGAGAACTTCAGCTGATGCGAGAG 215
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 43 CTGACAGTATGAGAACTTCCTCGCAACTTCAGAGAACTTCAGCTGATGCGAGAG 102
Oy 216 CTGGACACAGAGACGGAAGATTAAGAAAGCAGAGATTGACATCTGCTGACAGTACATC 275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 103 CTGGACACAGAGACGGAAGATTAAGAAAGCAGAGATTGACATCTGCTGACAGTACATC 162
Oy 276 TCCAGGTGAAGACGCTGCTCCAGACACGCGGTGAGCGCTGCGAGAAGATCCAGAAC 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 163 TCCAGGTGAAGACGCTGCTCCAGACACGCGGTGAGCGCTGCGAGAAGATCCAGAAC 222
Oy 336 GCCTACAGCAAGTGCAGAGAAATACAGTACGACAAAGTGCAGCTGCGCTGACAGACCTAC 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 223 GCCTACAGCAAGTGCAGAGAAATACAGTACGACAAAGTGCAGCTGCGCTGACAGACCTAC 282
Oy 396 GAGATGCTGATTAACACATTTGGAAGGCTTGTGATGCAAGCTGGCGGCTTTGAAGCAGAT 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 283 GAGATGCTGATTAACACATTTGGAAGGCTTGTGATGCAAGCTGGCGGCTTTGAAGCAGAT 342
Oy 456 CTGAAGAGCAAGATGAGAGGAGCATGATTTTGAAGCTCCGAGAGGCGAGGTTAAAAAAA 515
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 343 CTGAAGAGCAAGATGAGAGGAGCATGATTTTGAAGCTCCGAGAGGCGAGGTTAAAAAAA 402
Oy 516 GCCCGGGGTGCAGAAAGAAAAAGAGGTCGCCGGGCCGAGAGCAGAGCATCAGAGAA 575
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 403 GCCCGGGGTGCAGAAAGAAAAAGAGGTCGCCGGGCCGAGAGCAGAGCATCAGAGAA 462
Oy 576 GACACACCAAAAGAAAAAGAGCACAAGAGAGGTCTGAGTTCACTACACCATCTGCTGC 635
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 463 GACACACCAAAAGAAAAAGAGCACAAGAGAGGTCTGAGTTCACTACACCATCTGCTGC 522
Oy 636 GTGCACCCCTGTGATGCTGTGACATGCCGTGACCCCAAGCAACCCAGTACTGCTGC 695
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 523 GTGCACCCCTGTGATGCTGTGACATGCCGTGACCCCAAGCAACCCAGTACTGCTGC 582
Oy 696 TGCACACAGGTCTCTATGGGAGATGATGGCTGTGACATCCAGACTGCTCCAAATTGAG 755
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 583 TGCACACAGGTCTCTATGGGAGATGATGGCTGTGACATCCAGACTGCTCCAAATTGAG 642
Oy 756 TGGTTCACTTTGCTGCTGCTGACCTTACACAGAAACCCAAAGGAAATGCTTCTCCA 815
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 643 TGGTTCACTTTGCTGCTGCTGACCTTACACAGAAACCCAAAGGAAATGCTTCTCCA 702
Oy 816 CGGTGCTCCAGAAAGAAAGAGAAAGAGTAGAGAGAC-1GTGTGCCC -GGATCCGAG 873
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 703 CGGTGCTCCAGAAAGAAAGAGAAAGAGTAGAGAGACATGTGTGCCAGAGATCCGAG 762
Oy 874 GAGCAAGTTAATCTGCTCCCTTCAATTCGTGCAATATTTTCCCTTTTAAACTACC 933
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 763 GAGCAAGTTAATCTGCTCCCTTCAATTCGTGCAATATTTTCCCTTTTAAACTACC 822
Oy 934 TTGTTGGTTGATGATCTTAAGTAAAC 956
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 823 TTGTTGGTTGATGATCTTAAGTAAAC 845
```

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RESULT 11
US-09-442-013-9
; Sequence 9, Application US/09442013
; GENERAL INFORMATION:
```

```
; APPLICANT: Lou, Ying
; APPLICANT: Xu, Xiang
; APPLICANT: Xu, Cindy
; APPLICANT: Huang, Betty
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: NOVEL IAPs ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
; FILE REFERENCE: A-68289/DJB/RMS/DVA
; CURRENT APPLICATION NUMBER: US/09/442,013
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-442-013-9
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Query Match      67.6%; Score 647.4; DB 18; Length 958;
Best Local Similarity 99.1%; Pred. No. 1.9e-163;
Matches 651; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Oy 149 TGGAGGCTGATAGTATGAGAACCTTCCTGCGCAACTTCAGAGAACTTCAGCTGAT 208
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TGGTGGATTTACAGGTATGAGAACCTTCCTGCGCAACTTCAGAGAACTTCAGCTGAT 360
Oy 209 GCGAGAGCTGAGACCAAGAGCAGAAAGATTAAGAAAGCAGAGATTGACATCTGCTGACA 268
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 GCGAGAGCTGAGACCAAGAGCAGAAAGATTAAGAAAGCAGAGATTGACATCTGCTGACA 420
Oy 269 GTACATCTCCAGGTTGAAGACGCTGCTCCAGACACGCGCTGAGAGCGCTTCGAGAAAT 328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 GTACATCTCCAGGTTGAAGACGCTGCTCCAGACACGCGCTGAGAGCGCTTCGAGAAAT 480
Oy 329 CCAGAACGCGCTACAGCAAGTGCAGAAATACAGTACGACGCAAAAGTCCACTGCGCTTGA 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 CCAGAACGCGCTACAGCAAGTGCAGAAATACAGTACGACGCAAAAGTCCACTGCGCTTGA 540
Oy 389 GACCTACGAGATGATGATTAACACATTTGGAAGGCTTGTGATGCAAGCTGCGCGCTTTGA 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 GACCTACGAGATGATGATTAACACATTTGGAAGGCTTGTGATGCAAGCTGCGCGCTTTGA 600
Oy 449 AGCAGATCTGAAGGACAGATGAGAGGAGCATGATTTTGAAGGCTCCGAGGCGAGGTT 508
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 AGCAGATCTGAAGGACAGATGAGAGGAGCATGATTTTGAAGGCTCCGAGGCGAGGTT 660
Oy 509 AAAAAAGGCGGGGTGCAGAAAGAAAAAGAGGTCGCCGGGCCGAGAGCAGAGCATC 568
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 661 AAAAAAGGCGGGGTGCAGAAAGAAAAAGAGGTCGCCGGGCCGAGAGCAGAGCATC 720
Oy 569 AGAGGAAGACACACCAAGAAAAAGAGCACAAGAGAGGCTGATGTTCACTGACACCAT 628
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 721 AGAGGAAGACACACCAAGAAAAAGAGCACAAGAGAGGCTGATGTTCACTGACACCAT 780
Oy 629 CCGTCCGTCGACACCCCTGTGATGCTGTGACATGCCGTGGAACCCAAAGCAACCCACGTA 688
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 781 CCGTCCGTCGACACCCCTGTGATGCTGTGACATGCCGTGGAACCCAAAGCAACCCACGTA 840
Oy 689 CTGCTGTGTCACACAGGTCTCTATGGGAGATGATGGCTGTGACAAATCCAGACTGTC 748
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 841 CTGCTGTGTCACACAGGTCTCTATGGGAGATGATGGCTGTGACAAATCCAGACTGTC 900
Oy 749 AATGAGTGGTTCACTTTGCGCTGCTGAGACCTTACACAGAAACCCAAAGGAAATG 805
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 901 AATGAGTGGTTCACTTTGCGCTGCTGAGACCTTACACAGAAACCCAAAGGAAATG 957
```

```
RESULT 12
US-60-184-797-652
; Sequence 652, Application US/60184797
; GENERAL INFORMATION:
; APPLICANT: Hodgson, David M.
; APPLICANT: Lincoln, Stephen E.
; APPLICANT: Jones, Anissa L.
; APPLICANT: Yu, Jimmy Y.
```

APPLICANT: Russo, Frank D. Greenawalt, Lila B.
APPLICANT: Spitro, Peter A. Penzer, Scott R.
APPLICANT: Banville, Steve C. Roseberry, Ann M.
APPLICANT: Bratcher, Shawn R. Wright, Rachel J.
APPLICANT: Dufour, Gerard E. Chen, Wensheng
APPLICANT: Cohen, Howard J. Liu, Tommy
APPLICANT: Rosen, Bruce Yap, Pierre E.
APPLICANT: Shah, Purni Stockreher, Theresa K.
APPLICANT: Chalup, Michael S. Amshay, Stefan
APPLICANT: Hillman, Jennifer L. Fong, Willy Tuen
TITLE OF INVENTION: MOLECULES ASSOCIATED WITH GROWTH AND DEVELOPMENT
FILE REFERENCE: Pt-0114 P
CURRENT APPLICATION NUMBER: US/60/184,797
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: PERL Program
SEQ ID NO 652
LENGTH: 1275
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No: 121128.14
US-60-184-797-652

Query Match 67.4%; Score 645.6; DB 62; Length 1275;
Best Local Similarity 99.4%; Pred. No. 6.4e-163;
Matches 648; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 156 CTGATAGTATCGAGAACCTTCCCTGCGAATCTCAGAGAACTTCACGCTGATGCGAGAG 215
||| |||||
DB 56 CTGGACATATCGAAGAACCTTCCCTGCGAATCTCAGAGAACTTCACGCTGATGCGAGAG 115
OY 216 CTGACACGAGAGCGGAAGATTAAGAAAGAGATTGACATCTGGCTGCAGATACATC 275
||| |||||
DB 116 CTGGACCGAGAGCGGAAGATTAAGAAAGAGATTGACATCTGGCTGCAGATACATC 175
OY 276 TCCACGGTGAAGAGCGCTGCTCCAGACAGCGCGTGGAGCGCGCTGCAGAAAGTCCAGAAC 335
||| |||||
DB 176 TCCACGGTGAAGAGCGCTGCTCCAGACAGCGCGTGGAGCGCGCTGCAGAAAGTCCAGAAC 235
OY 336 GCCTACAGCAAGTGCAGAGAAATACAGTACGACGACAAAGTGCAGCTGGCCATGCGAGACTAC 395
||| |||||
DB 236 GCCTACAGCAAGTGCAGAGAAATACAGTACGACGACAAAGTGCAGCTGGCCATGCGAGACTAC 295
OY 366 GAGATGTTGATTAACACATTCGAAAGCTTGATGCGAGACCTGGCGCTTTGGAAGCAGAT 455
||| |||||
DB 296 GAGATGTTGATTAACACATTCGAAAGCTTGATGCGAGACCTGGCGCTTTGGAAGCAGAT 355
OY 466 CTGAAGGACAAAGATGAGAGGCGAGTATTTGAAAGCTCCGGGAGGCGAGGGTTAAAAAAA 515
||| |||||
DB 366 CTGAAGGACAAAGATGAGAGGCGAGTATTTGAAAGCTCCGGGAGGCGAGGGTTAAAAAAA 415
OY 516 GCGCGGGGTCAAGAAAAAGAGAGGTCCCGGGCCGAGGCGAGGAGGACATCAGAGGAA 575
||| |||||
DB 416 GCGCGGGGTCAAGAAAAAGAGAGGTCCCGGGCCGAGGCGAGGAGGACATCAGAGGAA 475
OY 576 GACACACCAAGAAAAAGAGACAAAGAGGCTCTGAGTTCTACTGACACCATCTCTGTC 635
||| |||||
DB 476 GACACACCAAGAAAAAGAGACAAAGAGGCTCTGAGTTCTACTGACACCATCTCTGTC 535
OY 636 GTGCACCCCTCTGATGTGTCGACATGCCCCGTGGACCCCAAGAACCCACGTAAGCCGTG 695
||| |||||
DB 536 GTGCACCCCTCTGATGTGTCGACATGCCCCGTGGACCCCAAGAACCCACGTAAGCCGTG 595
OY 696 TGCCACACAGGTCTCTATGGGAGATGATGGCTGTGCAATCCAGACTGTGCCAATTGAG 755
||| |||||
DB 596 TGCCACACAGGTCTCTATGGGAGATGATGGCTGTGCAATCCAGACTGTGCCAATTGAG 655
OY 756 TGGTTTCACTTTGCTGCGTGACCTTACACGAAACCCAAAGAAATGCT 807
||| |||||
DB 656 TGGTTTCACTTTGCTGCGTGACCTTACACGAAACCCAAAGAAATGCT 707

RESULT 13
US-60-278-258-16936
Sequence 16936, Application US/60278258
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
FILE REFERENCE: GX-0010-1 P
CURRENT APPLICATION NUMBER: US/60/278,258
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 17730
SOFTWARE: PERL Program
SEQ ID NO 16936
LENGTH: 1275
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No: 121128.14
US-60-278-258-16936

Query Match 67.4%; Score 645.6; DB 71; Length 1275;
Best Local Similarity 99.4%; Pred. No. 6.4e-163;
Matches 648; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 156 CTGATAGTATCGAAGAACCTTCCCTGCGAATCTCAGAGAACTTCACGCTGATGCGAGAG 215
||| |||||
DB 56 CTGGACATATCGAAGAACCTTCCCTGCGAATCTCAGAGAACTTCACGCTGATGCGAGAG 115
OY 216 CTGACACGAGAGCGGAAGATTAAGAAAGAGATTGACATCTGGCTGCAGATACATC 275
||| |||||
DB 116 CTGGACCGAGAGCGGAAGATTAAGAAAGAGATTGACATCTGGCTGCAGATACATC 175
OY 276 TCCACGGTGAAGAGCGCTGCTCCAGACAGCGCGTGGAGCGCGCTGCAGAAAGTCCAGAAC 335
||| |||||
DB 176 TCCACGGTGAAGAGCGCTGCTCCAGACAGCGCGTGGAGCGCGCTGCAGAAAGTCCAGAAC 235
OY 336 GCCTACAGCAAGTGCAGAGAAATACAGTACGACGACAAAGTGCAGCTGGCCATGCGAGACTAC 395
||| |||||
DB 236 GCCTACAGCAAGTGCAGAGAAATACAGTACGACGACAAAGTGCAGCTGGCCATGCGAGACTAC 295
OY 366 GAGATGTTGATTAACACATTCGAAAGCTTGATGCGAGACCTGGCGCTTTGGAAGCAGAT 455
||| |||||
DB 296 GAGATGTTGATTAACACATTCGAAAGCTTGATGCGAGACCTGGCGCTTTGGAAGCAGAT 355
OY 466 CTGAAGGACAAAGATGAGAGGCGAGTATTTGAAAGCTCCGGGAGGCGAGGGTTAAAAAAA 515
||| |||||
DB 366 CTGAAGGACAAAGATGAGAGGCGAGTATTTGAAAGCTCCGGGAGGCGAGGGTTAAAAAAA 415
OY 516 GCGCGGGGTCAAGAAAAAGAGAGGTCCCGGGCCGAGGCGAGGAGGACATCAGAGGAA 575
||| |||||
DB 416 GCGCGGGGTCAAGAAAAAGAGAGGTCCCGGGCCGAGGCGAGGAGGACATCAGAGGAA 475
OY 576 GACACACCAAGAAAAAGAGACAAAGAGGCTCTGAGTTCTACTGACACCATCTCTGTC 635
||| |||||
DB 476 GACACACCAAGAAAAAGAGACAAAGAGGCTCTGAGTTCTACTGACACCATCTCTGTC 535
OY 636 GTGCACCCCTCTGATGTGTCGACATGCCCCGTGGACCCCAAGAACCCACGTAAGCCGTG 695
||| |||||
DB 536 GTGCACCCCTCTGATGTGTCGACATGCCCCGTGGACCCCAAGAACCCACGTAAGCCGTG 595
OY 696 TGCCACACAGGTCTCTATGGGAGATGATGGCTGTGCAATCCAGACTGTGCCAATTGAG 755
||| |||||
DB 596 TGCCACACAGGTCTCTATGGGAGATGATGGCTGTGCAATCCAGACTGTGCCAATTGAG 655
OY 756 TGGTTTCACTTTGCTGCGTGACCTTACACGAAACCCAAAGAAATGCT 807
||| |||||
DB 656 TGGTTTCACTTTGCTGCGTGACCTTACACGAAACCCAAAGAAATGCT 707

```

RESULT 14
PCT-US01-04098A-646
; Sequence 646, Application PC/TUS0104098A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-029
; CURRENT APPLICATION NUMBER: PCT/US01/04098A
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: Not Yet Assigned
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/728,422
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/693,325
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/663,561
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/654,936
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/620,325
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 3960
; SOFTWARE: Custom
; SEQ ID NO 646
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (251)..(931)
PCT-US01-04098A-646

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Query Match          67.0%; Score 641.8; DB 1; Length 1465;
Best Local Similarity 98.9%; Pred. No. 7.1e-162;
Matches 646; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 156 CTGATAGTATCGAGAACTTCCCTCGGAATTCAGAGAACTTCAGTATCGAGAG 215
DB 281 CTGACAGATTCGAGAACTTCCCTCGGAATTCAGAGAACTTCAGTATCGAGAG 340
QY 216 CTGACACGAGGAGCGGAGATTAAGAAAGCAGAGATTGACATTCCTGGCTGCAGATCATC 275
DB 341 CTGACACGAGGAGCGGAGATTAAGAAAGCAGAGATTGACATTCCTGGCTGCAGATCATC 400
QY 276 TCCACGGTGAAGACGCTGTCTCCAGACACGCGGTGGAGCGCTGCAGAAATCCAGAAC 335
DB 401 TCCACGGTGAAGACGCTGTCTCCAGACACGCGGTGGAGCGCTGCAGAAATCCAGAAC 460
QY 336 GCCTACAGCAAGTGCAGAAATACAGTACGACAGCAAAAGTGCAGCTGGCCATGCAGACCTAC 395
DB 461 GCCTACAGCAAGTGCAGAAATACAGTACGACAGCAAAAGTGCAGCTGGCCATGCAGACCTAC 520
QY 396 GAATGTGATTAACACATTCGAGAGCTTGATGACAGACTGGCGCGCTTTGAAGCAGAT 455
DB 521 GAATGTGATTAACACATTCGAGAGCTTGATGACAGACTGGCGCGCTTTGAAGCAGAT 580
QY 456 CTGACAGCAAGATGAGGCGCAGTATTTTGAAGAGCTCCGAGAGCGAGGTTAAAAAAA 515
DB 581 CTGACAGCAAGATGAGGCGCAGTATTTTGAAGAGCTCCGAGAGCGAGGTTAAAAAAA 640
QY 516 GAGCGGGGTGAGAAAGAAAGAGGGTCCCGGGGCCGAGGAGCAGAGAGATCAGAGAA 575
DB 641 GAGCGGTGAGAAAGAAAGAGGGTCCCGGGGCCGAGGAGCAGAGAGATCAGAGAA 700
QY 576 GACACACCAAGAAAGAAAGAGAGAGGCTGAGTTCACTGACACATCTCTGTC 635

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DB 701 GACACACCAAGAAAGAAAGAGAGGCTGAGTTCACTGACACATCTCTGTC 760
QY 636 GTGACACCCCTGTGATGTGTGACATGCGGTGAGCCCAAGCAACCCAGTACGCTG 695
DB 761 GTGACACCCCTGTGATGTGTGACATGCGGTGAGCCCAAGCAACCCAGTACGCTG 820
QY 696 TGCCACGAGGTCTTCATGGGGAGATGATTTGGCTGTGACATCCAGACTGTCCAATTGAG 755
DB 821 TGCCACGAGGTCTTCATGGGGAGATGATTTGGCTGTGACATCCAGACTGTCCAATTGAG 880
QY 756 TGCTTTACCTTTGCTGCTGCGGTGACCTTACACAGCAACCCCAAGAAAGTGT 808
DB 881 TGCTTTACCTTTGCTGCTGCGGTGACCTTACACAGCAACCCCAAGAAAGTGT 933

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RESULT 15
US-09-620-325-298
; Sequence 298, Application US/09620325
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungling
; APPLICANT: Wang, Dunrui
; APPLICANT: Tillinghast, John
; APPLICANT: Dimanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 787CIP28
; CURRENT APPLICATION NUMBER: US/09/620,325
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: PL_FL-genes Version 1.0
; SEQ ID NO 298
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (251)..(931)
US-09-620-325-298

```

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Query Match          67.0%; Score 641.8; DB 24; Length 1465;
Best Local Similarity 98.9%; Pred. No. 7.1e-162;
Matches 646; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 156 CTGATAGTATCGAGAACTTCCCTCGGAATTCAGAGAACTTCAGTATCGAGAG 215
DB 281 CTGACAGATTCGAGAACTTCCCTCGGAATTCAGAGAACTTCAGTATCGAGAG 340
QY 216 CTGACACGAGGAGCGGAGATTAAGAAAGCAGAGATTGACATTCCTGGCTGCAGATCATC 275
DB 341 CTGACACGAGGAGCGGAGATTAAGAAAGCAGAGATTGACATTCCTGGCTGCAGATCATC 400
QY 276 TCCACGGTGAAGACGCTGTCTCCAGACACGCGGTGGAGCGCTGCAGAAATCCAGAAC 335
DB 401 TCCACGGTGAAGACGCTGTCTCCAGACACGCGGTGGAGCGCTGCAGAAATCCAGAAC 460
QY 336 GCCTACAGCAAGTGCAGAAATACAGTACGACAGCAAAAGTGCAGCTGGCCATGCAGACCTAC 395

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Db 461 GCCCTACAGCAAGTGCAGGAATACAGTAGCAGCAAAAGTGCAGCTGGCCATGCGAGACTAC 520
QY 396 GAGATGGTGGATTAACACATTGCAAGGCTTGATGCAAGACTGGCGCTTTGAAGCAGAT 455
|||||
Db 521 GAGATGGTGGATTAACACATTGCAAGGCTTGATGCAAGACTGGCGCTTTGAAGCAGAT 580
QY 456 CTGAAGGACAGATGAGGGGCGAGTATTTTGAAGCTCCGAGGGGCGAGGGTTAAAAANA 515
|||||
Db 581 CTGAAGGACAGATGAGGGGCGAGTATTTTGAAGCTCCGAGGGGCGAGGGTTAAAAANA 640
QY 516 GGGCGGGGTCAAGAAAAAGAGGGTCCGGGGCCGAGGCGAGGACATCAGAGGA 575
|||||
Db 641 GGGCTGGCTCAAGAAAAAGAGGGTCCGGGGCCGAGGCGAGGACATCAGAGGA 700
QY 576 GACAGACCAAGAAAAAGACACAAGAGAGGCTGAGTTCACTGACACCATCCTGTC 635
|||||
Db 701 GACAGACCAAGAAAAAGACACAAGAGAGGCTGAGTTCACTGACACCATCCTGTC 760
QY 636 GTGACCCCTCTGATGTGCTGACATGCCCGTGACCCCAACGCCACGTAATGCTG 695
|||||
Db 761 GTGACCCCTCTGATGTGCTGACATGCCCGTGACCCCAACGCCACGTAATGCTG 820
QY 696 TGCCACCAAGTCTCTATGGGAGATGATGGCTGTGACATCCAGACTGTCCAAATGAG 755
|||||
Db 821 TGCCACCAAGTCTCTATGGGAGATGATGGCTGTGACATCCAGACTGTCCAAATGAG 880
QY 756 TGGTTCACTTGGCTGGCTGACCTTACACGAAACCAAGGAAATGTT 808
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Db 881 TGGTTCACTTGGCTGGCTGACCTTACACGAAACCAAGGAAATGATT 933

Search completed: February 22, 2003, 22:02:55
Job time : 4166 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 20:16:33 : Search time 90 Seconds
(without alignments)
5978.339 Million cell updates/sec

Title: US-09-442-013-7
Perfect score: 958
Sequence: 1 ttgttgaccctcagcctgc.....cgtgtactactagtaacaa 958

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCr_NEM_PUB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEM_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	8487	10	US-09-764-877-3454	Sequence 3454, Ap
2	97	10.1	840	US-10-115-899-6	Sequence 6, Appli
3	97	10.1	1078	US-10-115-899-7	Sequence 7, Appli
4	75.8	7.9	754	US-09-731-872-187	Sequence 187, Ap
5	65.2	6.8	813	US-09-938-842A-1178	Sequence 1178, Ap
6	59.8	6.2	352	US-09-867-701-2399	Sequence 2399, Ap
7	52	5.4	953	US-09-801-368-257	Sequence 257, App
8	41.6	4.3	450	US-09-867-550-223	Sequence 223, App
9	41	4.3	846	US-09-867-550-1931	Sequence 1931, App
10	40	4.2	454	US-09-864-761-19549	Sequence 19549, A
11	39	4.1	451	US-09-854-133-146	Sequence 146, App
12	39	4.1	451	US-09-738-973-146	Sequence 146, App
13	37.8	3.9	398	US-09-960-352-8059	Sequence 8059, Ap
14	37.6	3.9	659158	US-09-771-208-20	Sequence 20, Appl
15	36.8	3.8	368	US-09-878-574-1665	Sequence 1665, Ap
16	36.8	3.8	387	US-09-878-574-1404	Sequence 1404, Ap
17	36.8	3.8	448	US-09-960-352-5218	Sequence 5218, Ap
18	36.8	3.8	643	US-09-764-869-577	Sequence 577, App
19	36.8	3.8	1329	US-09-815-242-4023	Sequence 4023, Ap

20	36.2	3.8	421	10	US-09-960-352-14430	Sequence 14430, A
21	36	3.8	415	10	US-09-960-352-2580	Sequence 2580, App
22	35.8	3.7	2153	10	US-09-822-849A-286	Sequence 286, App
23	35.8	3.7	3416	8	US-08-987-689A-1	Sequence 1, Appli
24	35.4	3.7	475	10	US-09-864-761-6203	Sequence 6203, Ap
25	35.4	3.7	511	10	US-09-864-761-22817	Sequence 22817, A
26	35.4	3.7	1209	10	US-09-815-242-9956	Sequence 9956, App
27	35	3.7	343	10	US-09-960-352-4500	Sequence 4500, Ap
28	34.4	3.6	420	10	US-09-960-352-9532	Sequence 9532, Ap
29	34.2	3.6	209	10	US-09-867-701-8665	Sequence 8665, Ap
30	34.2	3.6	266	9	US-10-040-739-902	Sequence 902, App
31	34	3.5	2105	10	US-09-999-678-1	Sequence 1, Appli
32	34	3.5	4796	10	US-09-764-847-1627	Sequence 1627, Ap
33	34	3.5	5835	9	US-09-927-597-1	Sequence 1, Appli
34	34	3.5	5937	9	US-09-927-597-3	Sequence 3, Appli
35	34	3.5	1337	10	US-09-764-846-312	Sequence 312, App
36	34	3.5	1337	10	US-09-764-847-1629	Sequence 1629, Ap
37	34	3.5	88421	9	US-09-976-059-1	Sequence 1, Appli
38	33.8	3.5	394	10	US-09-864-761-18958	Sequence 18958, A
39	33.6	3.5	215	10	US-09-867-701-9278	Sequence 9278, Ap
40	33	3.4	417	10	US-09-960-352-13113	Sequence 13113, A
41	33	3.4	462	10	US-09-149-721-2	Sequence 2, Appli
42	33	3.4	493	10	US-09-864-761-29936	Sequence 29936, A
43	33	3.4	599	10	US-09-864-761-13376	Sequence 13376, A
44	33	3.4	2489	10	US-09-764-864-552	Sequence 552, App
45	33	3.4	2504	10	US-09-764-864-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-09-764-877-3454
; Sequence 3454, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3454
; LENGTH: 8487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454

Query Match 11.8%; Score 113; DB 10; Length 8487;
Best Local Similarity 72.6%; Pred. No. 5.9e-23;
Matches 146; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY	657	GACATGCCGTGGACCAACGACCCAGCTGCTGTCGACACAGGTCTCTATGGG	716
DB	6700	GACCTCCCATGACGCCCAACGACCCAGCTGCTGTCGACACAGGTCTCTATGGG	6759
QY	717	GAGATGATTGCTGTGACAACTGCTCCAAATGATGATGTTTCACTTCCCTGCGTG	776
DB	6760	GAGATGATGGCTGGCAACGACGAGTCCCATGATGATGTTTCACTTCCCTGCGTG	6819
QY	777	GACCTTACCAACCAACCAAGAAATGTTCTGTCACGCTGTGTCCAGAAAAGAG	836
DB	6820	GGGCTCAATCAATCAATCAACCAAGGCAAGTGTACTGTCCCAAGTGGCGGGGGAACGAG	6879
QY	837	AAGAAAGATAGAGAGCTG	857
DB	6880	AAGACCATGACAAAGCCCTG	6900
RESULT 2			
US-10-115-899-6			

```
; Sequence 6, Application US/10115899
; Patent No. US20020151025A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/10/115,899
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
US-10-115-899-6

Query Match          10.1%; Score 97; DB 12; Length 840;
Best Local Similarity 68.9%; Pred. No. 9.5e-19;
Matches 133; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 655 TGCACATGCCGTGACCCCAACGACGCTACTGCTGTCGCCACGAGTCTCTATG 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 608 TTGAGTTTGCATATAGATCCATATGAACTCATGCTATGCAACCAAGTCTTATG 667

QY 715 GGGAGATGATGGCTGGAATCCAGACCTGCTCAATGTGTTGCTTCACTTGGCCG 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 668 GGGAGATGATGAGATGACATGACAGTGTCCATGTGATGCTTTCATGATG 727

QY 775 TGACCTTACACGAAACCAAGAAATGTTCTGTCCAGCGTGTCCAGAAAGA 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 728 TTTCACCTTACCTTAAACCAAGGGAATGTATTGCCCAAGTGCAGGAGATATATG 787

QY 835 GGAAGAAGAAGTA 847
    ||| ||| |||
DB 788 AGAAACAATGGA 800

RESULT 3
US-10-115-899-7
; Sequence 7, Application US/10115899
; Patent No. US20020151025A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/10/115,899
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
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; NAME/KEY: CDS
; LOCATION: (92)..(931)
US-10-115-899-7

Query Match          10.1%; Score 97; DB 12; Length 1078;
Best Local Similarity 68.9%; Pred. No. 1.1e-18;
Matches 133; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 655 TGCACATGCCGTGACCCCAACGACGCTACTGCTGTCGCCACGAGTCTCTATG 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 699 TTGAGTTTGCATATAGATCCATATGAACTCATGCTTATGCAACCAAGTCTTATG 758

QY 715 GGGAGATGATGGCTGTCGACATCCAGACTGTCCAAATGAGTGTTCCTTGGCCG 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 759 GGGAGATGATGAGATGACATGACAGTGTCCAAATGATGTTTCACTTTCATGTG 818

QY 775 TGACCTTACACGAAACCAAGAAATGTTCTGTCCAGCGTGTTCAGAAAGA 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 819 TTTCACCTTACCTTAAACCAAGGGAATGTATTGCCCAAGTGCAGGAGATATATG 878

QY 835 GGAAGAAGAAGTA 847
    ||| ||| |||
DB 879 AGAAACAATGGA 891

RESULT 4
US-09-731-872-187/c
; Sequence 187, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouquelier, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US.3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 187
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 181..462
US-09-731-872-187

Query Match          7.9%; Score 75.8; DB 10; Length 754;
Best Local Similarity 75.7%; Pred. No. 1.6e-12;
Matches 137; Conservative 0; Mismatches 32; Indels 12; Gaps 3;

QY 776 GGACCTTACCAAGCAAAACCAAGAAATGTTCTGTCCAGCGTGTCCAGAAAGAG 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 294 GGACCTTACCATG-AATCCAGAGGAATGCTGTCTCCAGCGTGTCCAGAAAGAG 236

QY 836 GAAGAAGAAGTAGAGAGCTGTGTCGCCGATCCAGAGCAAGTTAATGTGCTCC 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 GAAGAAG--GAAGAAGAAGCTGTATGCGAGATCAAG-----AGCTATCTCTTT 187

QY 896 ATTCGTGTCCCAATATTTCCTCTTAAACTACTGTTGCGTGTATATCTAGTAA 955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 186 ATTCATGTTCAGAGATTCTTTCATTTAAACTACTGTTCAATGATATGATATAA 127

QY 956 C 956
    |
DB 126 C 126
```

```
RESULT 5
US-09-938-842A-1178
: Sequence 1178, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIPI300-3
: CURRENT APPLICATION NUMBER: US/09/938, 842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227, 866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264, 647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300, 111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 1178
: LENGTH: 813
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-1178

Query Match          5.8%; Score 65.2; DB 9; Length 813;
Best Local Similarity 67.7%; Pred. No. 2.3e-09;
Matches 107; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

Oy 657 GACATGCCCGGAGCCCAAGCAAGCCACGTCGCTGTCACCAAGTCTCTATGGG 716
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 550 GAGCAGCCAAATGATGCAACGACCAACTACTGTGTCACAGGTGCTCTTTGGA 609
Oy 717 GAGATGATTTGGCTGTGACATCCAGACTGTC--CAATTGAGTGGTTTCACTTGCCTGC 773
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 610 GACATGATTTGGCTGTGACATGAGATTGCCAAGAGGATGTTTCATATACATGC 669
Oy 774 GTGACCTTACCAGCAACCCCAAGGAAGAAATGTTCTG 811
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 670 GTTGGCTTCACACTGAGACGAGATTCAAGGGAATG 707

RESULT 6
US-09-867-701-2399
: Sequence 2399, Application US/09867701
: Patent No. US20020132237A1
: GENERAL INFORMATION:
: APPLICANT: Agiate, Paul A.
: APPLICANT: Jones, Robert
: APPLICANT: Harlocker, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.497
: CURRENT APPLICATION NUMBER: US/09/867, 701
: CURRENT FILING DATE: 2001-05-29
: NUMBER OF SEQ ID NOS: 10912
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2399
: LENGTH: 352
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(352)
: OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2399

Query Match          6.2%; Score 59.8; DB 10; Length 352;
Best Local Similarity 50.9%; Pred. No. 5.8e-08;
Matches 139; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
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Oy 156 CTGATAGCTATCGAGAACCTTCCCTGCGAACTTCAGAGAACTTCCAGCTGATGCGAG 215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 CTGAAATGATTTGACACACTTCTCTATGATCTGCGGACCACTTTCAGCGAATGGCGAG 139
Oy 216 CTGACAGAGAGCAGGAAGATAGAAAGCAGAGATTGACATCTGCTGCGAGATACATC 275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 ATGACACTGACAGTGCAGAAATTAATTGGATCACTAGAAACAAGAGTCAGTAATTTCTT 199
Oy 276 TCACAGGTGGAAGACCGCTGCTCCAGACACGCGCTGAGCGCCCTGCACAAATCCAGAC 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 ATGAATGGAAGAAATAAATAAATTAACCTGAGTGGAGGGGAAGAGCAATGCAATCCATAAAAA 259
Oy 336 GCCTACAGCAAGTGCAGGAATATACAGTGCAGCAAGATGCAAGTGCATGAGAGCTAC 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 260 GACTACTATTAAGCTTTTGGAAAGATGCAATGAGAAAGTTTCACTTGGCAACCAAGATATAT 319
Oy 396 GAGATGTGTGATTAACACATTCGAAGCTTGAT 428
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 GACTTGTATGATCGACACTTGAGAAAGCTGAT 352
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```
RESULT 7
US-09-801-368-257
: Sequence 257, Application US/09801368
: Patent No. US20020128250A1
: GENERAL INFORMATION:
: APPLICANT: Busby, Robert
: APPLICANT: Call, Brian
: APPLICANT: Hecht, Peter
: APPLICANT: Holtzman, Doug
: APPLICANT: Madden, Kevin
: APPLICANT: Maxon, Mary
: APPLICANT: Milne, Todd
: APPLICANT: No. US20020128250A1man, Thea
: APPLICANT: Royer, John
: APPLICANT: Salama, Sofie
: APPLICANT: Sherman, Amir
: APPLICANT: Silva, Jeff
: APPLICANT: Summers, Eric
: TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
: FILE REFERENCE: 109272.147
: CURRENT APPLICATION NUMBER: US/09/801, 368
: CURRENT FILING DATE: 2001-03-07
: PRIOR APPLICATION NUMBER: US 09/487, 558
: PRIOR FILING DATE: 2000-01-19
: PRIOR APPLICATION NUMBER: US 60/160, 587
: PRIOR FILING DATE: 1999-10-20
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 257
: LENGTH: 993
: TYPE: DNA
: ORGANISM: Saccharomyces cerevisiae
US-09-801-368-257
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Query Match          5.4%; Score 52; DB 10; Length 993;
Best Local Similarity 59.5%; Pred. No. 2e-05;
Matches 88; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Oy 664 CCGTGAGCCCAAGCAAGCCAGTACTGCTGTGACCAGGCTCTCATGGGAGATGA 723
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 821 CCAAGACTAGCGCGACACCGCTCTACTGCTACTGTAACCAATGCGCATAGGGGAAATGG 880
Oy 724 TTGCTGTGACAAATCGACACTGTCCAAATGAGTGTTCCTTTCCTTGCCTGAGCTTA 783
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 881 TGGGCTGTGATGGCGCAGACTGTGAGTAATGATGTTCCATTTGCCATGTATTGACTCG 940
Oy 784 CCACGAACCCCAAGGAATATGTTCTG 811
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 941 AAAGTCTACCTAAGGGAAGTGTATTG 968
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RESULT 8

```
US-09-867-550-223
; Sequence 223, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(31)
; OTHER INFORMATION: wherein any n is one of a or t or g or c
US-09-867-550-223
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Query Match 4.3%; Score 41.6; DB 10; Length 450;
Best Local Similarity 50.2%; Pred. No. 0.016;
Matches 101; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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QY 201 CAGCTGATGGAGAGCTGGACGAGAGGAGATGAAGAAACGACAGATTGACATCTG 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 CGGCTNTACCCACATCGAGTGGAAATCGCGGTATCGAGTGGAGAGCCCATCCG 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 261 GCTGACAGTACATCTCCAGCGTGAAGACGCTGTCTCCAGACCAGCGCGTGAAGCCCTG 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 AACCGGTGAAGCGGAGATGAGAGAGCGACGCGGAATACCTCAACGACGAGAT 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 321 CAGAAATCCAGAACCCCTACAGCAAGTAGTACAGTACAGCAAAATGTCAGCTG 380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 AAGCGCATCCAGAAAGAGCTCGCGGAGGAGAGAGCGCGGACGAGACCGCGGAGATC 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 381 GCCATGCAGACTACGAGATG 401
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 GAGGAGAAAGTCAAGAGACG 225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-09-867-550-1931
; Sequence 1931, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1931
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-550-1931
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Query Match 4.3%; Score 41; DB 10; Length 846;
Best Local Similarity 50.8%; Pred. No. 0.033;
Matches 98; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 468 ATGAGGCGAGTATTTTGAAGCTCCGAGGCGGAGGTTAAAAAAGCCGGGTGAG 527
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 AGGTGTATTAATCATGTAAGAGTCTTGAAGCCGACGCTTAATTAAGGACATGTGA 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 528 AAGAAAAAAGAGGTCGCCGGCGGAGGAGGACATCAGAGAACACACCAAG 587
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 GAGAAAGTTCTTGGCTACAGGCGGAGACCTGAGAACCGGAAGGTAAAGACATGAGT 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 588 AAAAAGACCAAGAGAGGCTGTGATTCATGACCATCTGTCGCCCTGACCCCTCT 647
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 556 GCAGTACAGCCACAAACAGAGTAGTAGACATTCATCCAGCTTTTGGGGCCACTCT 615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 648 GATGTCTGACCA 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 616 TATCTATGAGACA 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 10
US-09-864-761-19549/c
; Sequence 19549, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
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SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19549
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006371.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9
; OTHER INFORMATION: EST_HUMAN HIT: AW900281.1, EVALUE 7.30e+02
; OTHER INFORMATION: NT HIT: Y12488.1, EVALUE 4.50e+00
; OTHER INFORMATION: SWISSPROT HIT: O68827, EVALUE 7.80e+00
US-09-864-761-19549

Query Match 4.2%; Score 40; DB 10; Length 454;
Best Local Similarity 48.7%; Pred. No. 0.047;
Matches 109; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

OY 384 ATGCAGACCTAGCAGATGTGATTAACCATTCGAGGCTTGATGCAGACCTGGCGCC 443
DB 451 AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
OY 444 TTGGAAGCAGATCTGAGAGCAAGATGAGGCGCAGTATTGAAAGCTCCGAGGCGCA 503
DB 391 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 332
OY 504 GGGTTAAAAAGGCCGGGCTCAGAAAGAAAAAGAGGGTCCCGGGCCGAGCAGAGAG 563
DB 331 GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 272
OY 564 ACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
DB 271 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 228

RESULT 11
US-09-854-133-146
; Sequence 146, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854.133
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-146

Query Match 4.1%; Score 39; DB 9; Length 451;
Best Local Similarity 48.5%; Pred. No. 0.092;
Matches 146; Conservative 0; Mismatches 145; Indels 10; Gaps 1;
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OY 221 CCAGAGAGAGAGAGATTAAGAAAGCAGAGATGCATCTGGCTGAGAGATCATCCAC 280
DB 73 CGCGAATATACCAAGAGATCTTCAAGAGAGCTTAACACAGTCTTACGAGCGTTAGTCGCA 132
OY 281 GGTGAAGAGCGTGTCTCCAGACCGCGTGGAGCGCTTCAGAAAGATCCAGAGCGCTA 340
DB 133 GACAGACGGGGGCGCAAGACGGCGGATGCTGCATGTGTGACAGCGCGGCTGATCCGCAC 192
OY 341 CAGCAAGTCAAGGAATACAGTGCAGACAAAGTGCAGCTGGCCATGCAGACCTACGAGAT 400
DB 193 CAGGAGCTG-----GGCGAGAGAAAGATCCAGATCTGCAGACCAAGATGTTGAGCT 242
OY 401 GGTGATTAACACATTTCGAAGGCTTGATGCAGACCGCGCGCTTGAAGCAGATCTGAA 460
DB 243 GGTGAGAAACCCACGCGGCGAGGTGCACGCCACCTGGAGCTGTTCGAGGCGCAGCAGCA 302
OY 461 G 461
DB 303 G 303

RESULT 12
US-09-738-973-146
; Sequence 146, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indrias, Carol Joseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliott, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738.973
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-738-973-146

Query Match 4.1%; Score 39; DB 10; Length 451;
Best Local Similarity 48.5%; Pred. No. 0.092;
Matches 146; Conservative 0; Mismatches 145; Indels 10; Gaps 1;
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Db 243 GGTGGAAACCGACGCGGAGGTGGACACCGCTGGAGCTGTGAGGCGCAGCAGGA 302
 Oy 461 G 461
 Db 303 G 303

RESULT 13

US-09-960-352-8059
 : Sequence 8059, Application US/09960352
 : Patent No. US20020137139A1

GENERAL INFORMATION:
 : APPLICANT: Wairren, Wesley C.
 : APPLICANT: Tao, Nengbing
 : APPLICANT: Byatt, John C.
 : APPLICANT: Mathalagan, Nagappan
 : TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 : FILE REFERENCE: 16511.006/37-21(10298)C
 : CURRENT APPLICATION NUMBER: US/09/960,352
 : CURRENT FILING DATE: 2001-09-24
 : NUMBER OF SEQ ID NOS: 15112
 : SEQ ID NO 8059
 : LENGTH: 398
 : TYPE: DNA
 : ORGANISM: Bos taurus
 : OTHER INFORMATION: Clone ID: 35-BOVMS1-019-Q1-E1-A4
 : US-09-960-352-8059

Query Match 3.9%; Score 37.8; DB 10; Length 398;
 Best Local Similarity 46.4%; Pred. No. 0.19;
 Matches 123; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Oy 216 CTGGACCAAGAGGAGATAGAAAGCAGCATGACATCTGCTGAGAGTACATC 275
 Db 48 CAGGAAGCTGCAACGAGAGAAAGCCAGAGGCTCATGATGAGCCATGATG 107
 Oy 276 TCCAGCGTGAAGAGCTGTCTCCAGACACGCGTGGAGCGCTGAGAGATCCAGAAC 335
 Db 108 GCTGAGGAGCTGAAGAAGAGCAGACACCGAGCGCCACTGAGAGGATGAAGAAGAAC 167
 Oy 336 GCCTACAGCAGTGCAGAGATACAGTACAGACAAAGTGCAGTGGCCATGACAGACTAC 395
 Db 168 ATGAGAGAGCGGTGAAGAGCTGACAGAACGCTGTGATGAGGCTGAGAGTGGCCCTG 227
 Oy 396 GAGATGTGATTAACACATTCGAGAGCTGATGAGAGCTGGCGGCTTTGAAGCAGAT 455
 Db 228 AAGGCGGGAAGAGCAGATCCAGAACTGGAGGCCAAGGTGCTGAGCTGGAAGGAGAG 287
 Oy 456 CTGAAGGACAAAGATGAGAGGCACTG 480
 Db 288 GTATAGAGTACGAGAAAGCGCAATG 312

RESULT 14

US-09-771-208-20/C
 : Sequence 20, Application US/09771208
 : Patent No. US20020155564A1

GENERAL INFORMATION:
 : APPLICANT: MEDRANO, JUAN
 : APPLICANT: BRADFORD, ERIC
 : APPLICANT: HORVAT, SIMON
 : TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
 : FILE REFERENCE: 407T-923710US
 : CURRENT APPLICATION NUMBER: US/09/771,208
 : CURRENT FILING DATE: 2001-01-26
 : PRIOR APPLICATION NUMBER: US 08/999,477
 : PRIOR FILING DATE: 1997-12-29
 : NUMBER OF SEQ ID NOS: 20
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 20
 : LENGTH: 659158

TYPE: DNA
 : ORGANISM: Mus musculus
 : FEATURE:
 : NAME/KEY: misc.feature
 : LOCATION: (123459)..(123478)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (602466)..(602485)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (546998)..(547017)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (494715)..(494814)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (390986)..(391005)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (346860)..(346823)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (317174)..(317193)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (280353)..(280373)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (271829)..(271848)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (183872)..(183891)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (170625)..(170645)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : LOCATION: (132680)..(132700)
 : OTHER INFORMATION: n is unidentified a, c, g, or t
 : NAME/KEY: misc.feature
 : OTHER INFORMATION: n is a, c, g, or t
 : US-09-771-208-20

Query Match 3.9%; Score 37.6; DB 9; Length 659158;
 Best Local Similarity 45.1%; Pred. No. 10;
 Matches 139; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Oy 167 CGGAACCTTCCCTGCGAATTCAGAGAACTTCCAGCTGATGCGAGAGCTGGACAGAG 226
 Db 251205 CCGGAACCTTCCCTGCGAATTCAGAGAACTTCCAGCTGATGCGAGAGCTGGACAGAG 251146
 Oy 227 GAGGGAAGATGAAGAGCAGAGATGACATCTGCTGACAGATACATCTCCAGGTGA 286
 Db 251145 GAAGGCAAGGTAGATGGAGGCTTTAGAGAGGAAGAGAGAGAGAGAGAGAGAG 251086
 Oy 287 GAGCGTGTCTCCAGACCGCGCTGGAGCGCTTCAGAAAGATCCAGAACGCCCTACAGCAA 346
 Db 251085 GGAGCAG 251026
 Oy 347 GTGCAAGGAATACAGTGCAGACAAAGTGCAGCTGGCCATGCGAGACTTACGAGATGTTGGA 406
 Db 251025 GGAGGAG 250966
 Oy 407 TAAACACATTGCAAGGCTTGATGCAAGCTGGCGGCTTTGAAGCAGATCTGAAGAGACA 466
 Db 250965 GGAGCAG 250906
 Oy 467 GATGAGAG 474
 Db 250905 GGAGGAGG 250898

RESULT 15

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/258,372
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/751,230
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mooi, Leslie A.
 REGISTRATION NUMBER: 37,047
 REFERENCE/DOCKET NUMBER: 028722-144
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-7400
 TELEFAX: 415-854-8275
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1902 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: . cdna
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 109..741
 US-09-258-372-1

	Query Match	11.8%	Score 113	DB 4	Length 1902
	Best Local Similarity	72.6%	Pred. No. 2e-24		
	Matches 146	Conservative 0	Mismatches 55	Indels 0	Gaps 0
QY	657	GACATGCCCGTGGACCCAAACGACCGATGCTCCTGTGACACAGGTCCTATGGG	716		
Db	505	GACCTCCCCATTCGACCCCAACGACCCCGATCTGTCTGCAACGAGTCCTATGGG	564		
QY	717	GAGATGATGGGTGGTGACAAATCCAGACGTCCCAATGTGGTTCACCTTGCCGCGGG	776		
Db	555	GAGATGATCGGCTGGGACACACGACGATGCCCATGTGATGGTTCACCTTCGTGGG	624		
QY	777	GACCTTACACGAAACCCAAAGAAATGTTCTCTCCAGCTGTGTCTCCAGAAAGAGG	836		
Db	625	GGGCTCATCATAAACCCAAAGGGCAAGTGTACTGTCCCAAGTGCCTGGGGGAGAACGAG	684		
QY	837	AAGAAGATGAGAGAGAGCTG	857		
Db	685	AAGACCATGACAAAGCCCTG	705		

RESULT 11
 US-09-258-371-9
 Sequence 9, Application US/09258371
 Patent No. 5986078
 GENERAL INFORMATION:
 APPLICANT: Garkavtsev, Igor
 APPLICANT: Rihabowol, Karl
 TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
 TITLE OF INVENTION: SUPPRESSOR GENE INGI
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
US-09-258-371-9

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	Query Match	11.8%	Score 113	DB 2	Length 2061
	Best Local Similarity	72.6%	Pred. No. 2,1e-24		
	Matches 146	Conservative 0	Mismatches 55	Indels 0	Gaps 0
QY	657	GACATGCGCCGTGGAGCCCAAGCAAGCCACGATGCTCTGTGCGCACCAGGTCTCTATGGG	716		
DB	664	GACCTCCCATTCGACCCCAAGCAAGCCACGATGCTCTGTGCAACAGATCTCTATGGG	723		
QY	717	GAGATGATGGGTGGATCCAAATCCAGATGCTCCAAATGATGGGTTCACATTGSCCTGGCGG	776		
DB	724	GAGATGATCGGTGGGCAACAGACAGATGGCCCATCGAGATGGTCTTCACACTCTCTGTGGCGG	783		
QY	777	GACCTTACACAGAAACCCAAAGAAATGTTCTGTCCAGCGTGTGCCAGAAAAAGAG	836		
DB	784	GGGCTTCATTCATTAACCCAAAGGGCAAGTGACTGTCCCAAGTGCGGGGGAGAAAGAG	843		
QY	837	AAGAAAGATGAGAGGACCTG	857		
DB	844	AAGACCATGACAAAGCCCTG	864		

RESULT 12
 US-08-751-230-9
 Sequence 9, Application US/08751230
 Patent No. 6117633
 GENERAL INFORMATION:
 APPLICANT: Garkavtsev, Igor
 APPLICANT: Riabowol, Karl
 TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
 TITLE OF INVENTION: SUPPRESSOR GENE INGI
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/751,230
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 514


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Qy      837  AAGAAGTAGGAGGAGCTG  857
          ||| | | | | |
Db      577  AAGACCATGGACAAGCCCTG  597

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RESULT 4
US-09-00

; Sequence 4, Application US/09006783A
; Patent No. 6297366

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; GENERAL INFORMATION:
; APPLICANT: Gudkov

```

APPLICANT: Garkavstev, Igor
APPLICANT: Riabov, Karl

TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
TITLE OF INVENTION: Pathway

; NUMBER OF SEQUENCES: /
; CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen H
STREET: 300 South Wacker Drive

CITY: Chicago
STATE: Illin
COUNTRY: USA

```

;      ZIP: 60606
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Ejectable Disk

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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, V
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/006,7
FILING DATE: 15-JAN-1998

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: NO. 6297366nan, Kev
REGISTRATION NUMBER: 35,3
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION
TELEPHONE: 312-913-0000

TELEPHONE: 312-913-
TELEFAX: 312-913-
INFORMATION FOR SEQ ID

```

; SEQUENCE CH
; LENGTH:

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?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: CDNA
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 7..813
?      US-09-006-783A-4

```

RESULT 5

US-09-258-257-1

; Sequence 1, Application US/09258257
; Patent No. 5965398

```

; GENERAL INFORMATION:
; APPLICANT: GARKAV

```

APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR

```

; TITLE OF INVENTION: SUP
; NUMBER OF SEQUENCES: 12
CORRESPONDING ADDRESSES

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P O Box 1404

CITY: Alexandria
STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404

```

;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk

```

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;
;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE:  patentIn Release #1.0, Ver
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  ITS/00/358 357

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APPROVAL: 05/03/2004
FILING DATE:
CLASSIFICATION:

; CENDEX INFORMATION;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08

FILING DATE: 08-DEC-
ATTORNEY/AGENT INFORMAT

NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37, 04

REFERENCE
TELECOMMUN
EDITION

```

? TELEPHONE: (630) 834-7400
? TELEFAX: (650) 854-8275
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1902 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 109..738
? OS-09-258-257-1

```

GENE

US-09-258-371-1
; Sequence 1, Application US/09258371
; Patent No. 5986078
; GENERAL INFORMATION:

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 19:24:43 : Search time 69 Seconds
(without alignments)
4257.918 Million cell updates/sec

Title: US-09-442-013-7
Perfect score: 958
Sequence: 1 ttgtgacctgacccctgc.....cgtgtgactagttaacaa 958

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCtUS_COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfillseq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	636.8	66.5	678	US-09-195-286-3	Sequence 3, Appli
2	636.8	66.5	699	US-09-195-286-2	Sequence 2, Appli
3	113	11.8	633	US-09-006-783A-6	Sequence 6, Appli
4	113	11.8	873	US-09-006-783A-4	Sequence 4, Appli
5	113	11.8	1902	US-09-258-257-1	Sequence 1, Appli
6	113	11.8	1902	US-09-258-371-1	Sequence 1, Appli
7	113	11.8	1902	US-08-568-721A-1	Sequence 1, Appli
8	113	11.8	1902	US-08-751-230-1	Sequence 1, Appli
9	113	11.8	1902	US-09-499-082-1	Sequence 1, Appli
10	113	11.8	1902	US-09-258-372-1	Sequence 1, Appli
11	113	11.8	2061	US-09-258-371-9	Sequence 9, Appli
12	113	11.8	2061	US-08-751-230-9	Sequence 9, Appli
13	113	11.8	2061	US-09-499-082-9	Sequence 9, Appli
14	113	11.8	2061	US-09-258-372-9	Sequence 9, Appli
15	113	11.8	2061	US-09-006-783A-2	Sequence 2, Appli
16	113	11.8	2061	US-09-159-871-1	Sequence 1, Appli
17	97	10.1	840	US-09-601-478-6	Sequence 6, Appli
18	97	10.1	1078	US-09-601-478-7	Sequence 7, Appli
19	97	10.1	1154	US-09-484-970B-81	Sequence 81, Appli
20	75.8	7.9	7218	US-08-232-463-14	Sequence 14, Appli
21	46.8	4.9	289	US-09-007-005-17	Sequence 17, Appli
22	46.8	4.9	289	US-09-244-796-17	Sequence 17, Appli
23	41.4	4.3	2338	US-08-425-069-1	Sequence 1, Appli
24	41.4	4.3	2338	US-08-317-844B-1	Sequence 1, Appli
25	40.2	4.2	277	US-09-007-005-3	Sequence 3, Appli
26	40.2	4.2	277	US-09-244-796-3	Sequence 3, Appli
27	39.8	4.2	248	US-09-007-005-32	Sequence 32, Appli

28	39.8	4.2	248	4	US-09-244-796-32	Sequence 32, Appli
29	39	4.1	451	4	US-09-370-838-146	Sequence 146, App
30	37.8	3.9	1995	2	US-08-425-069-3	Sequence 3, Appli
31	37.8	3.9	1995	2	US-08-317-844B-3	Sequence 3, Appli
32	37.4	3.9	3588	1	US-08-197-792-32	Sequence 32, Appli
33	37.4	3.9	3588	1	US-08-459-850-32	Sequence 32, Appli
34	37.4	3.9	3588	1	US-08-459-850-32	Sequence 32, Appli
35	36.2	3.8	51259	3	US-08-781-891-209	Sequence 209, App
36	35.8	3.7	3416	2	US-08-357-642A-2	Sequence 2, Appli
37	35.8	3.7	3416	2	US-08-460-626-2	Sequence 2, Appli
38	35	3.7	1926	4	US-09-249-585A-4	Sequence 4, Appli
39	35	3.7	1931	2	US-09-130-114-2	Sequence 2, Appli
40	35	3.7	2576	1	US-08-471-033-35	Sequence 35, Appli
41	35	3.7	2576	2	US-08-471-044-35	Sequence 35, Appli
42	35	3.7	2576	2	US-08-463-483A-35	Sequence 35, Appli
43	35	3.7	2576	2	US-08-471-046A-35	Sequence 35, Appli
44	35	3.7	2576	2	US-08-470-566B-35	Sequence 35, Appli
45	35	3.7	2576	2	US-08-469-334-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1
US-09-195-286-3
: Sequence 3, Application US/09195286
: Patent No. 6066474
: GENERAL INFORMATION:
: APPLICANT: Marcu, Kenneth B.
: TITLE OF INVENTION: Y2H56 A STRONG IKK BINDING PROTEIN
: FILE REFERENCE: Docket No. 6066474 178-258
: CURRENT APPLICATION NUMBER: US/09/195,286
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 678
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-195-286-3

Query Match 66.5%, Score 636.8; DB 3; Length 678;
Best Local Similarity 98.9%; Pred. No. 1.4e+183;
Matches 641; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY	156	CTGATAGTATCGAGAACCTTCCTCGCAACTTCAGAGAACTTCACCTGATGCGAAG	215
DB	31	CTGGACAGTATCGACACCATCCCGCGAACCTTCAGAGAACTTCACCTGATGCGAAG	90
QY	216	CTGGACAGAGAGCGAAGATAGAAAGCAGAGATTGACATCTGGTCGAGATATC	275
DB	91	CTGGACAGAGAGCGAAGATAGAAAGCAGAGATTGACATCTGGTCGAGATATC	150
QY	276	TCCACGCTGAGAGACGCTCTCCAGACAGCGCGTGAGCGCGCTGCAGAAATCCAGAC	335
DB	151	TCCACGCTGAGAGACGCTCTCCAGACAGCGCGTGAGCGCGCTGCAGAAATCCAGAC	210
QY	336	GCCTACACAGTGCAGAGATACAGTACAGCAAGAGTGCAGCTGGCCATGCAGACCTAC	395
DB	211	GCCTACACAGTGCAGAGATACAGTACAGCAAGAGTGCAGCTGGCCATGCAGACCTAC	270
QY	396	GAGATGGGTGAACACATTCGAAAGGCTTGATGACAGACCTGGCGCTTTGAAGCAGAT	455
DB	271	GAGATGGGTGAACACATTCGAAAGGCTTGATGACAGACCTGGCGCTTTGAAGCAGAT	330
QY	456	CTGAAGCAAGATGAGAGCGAGTATTTGAAAGCTCCGAGAGCGAGGTTAAAAAAA	515
DB	331	CTGAAGCAAGATGAGAGCGAGTATTTGAAAGCTCCGAGAGCGAGGTTAAAAAAA	390
QY	516	GCCCGGGTCAAGAAAGAGAGGTTCCCGGGCCGAGGAGAGGACATCAGAGGAA	575
DB	391	GCCCGGGTCAAGAAAGAGAGGTTCCCGGGCCGAGGAGAGGACATCAGAGGAA	450